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<b>(54) Title:</b> NOVEL BACTERIAL POLYPEPTIDES AND POLYNUCLEOTIDES		
<b>(57) Abstract</b>  <p>This invention relates to newly identified Streptococcal polynucleotides, polypeptides encoded by such polynucleotides, the uses of such polynucleotides and polypeptides, as well as the production of such polynucleotides and polypeptides and recombinant host cells tranformed with the polynucleotides. This invention also relates to inhibiting the biosynthesis or action of such polynucleotides or polypeptides and to the use of such inhibitors in therapy.</p>		

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## NOVEL BACTERIAL POLYPEPTIDES AND POLYNUCLEOTIDES

### FIELD OF THE INVENTION

This invention relates to newly identified polynucleotides and polypeptides, and their production and uses, as well as their variants, agonists and antagonists, and their uses. In particular, in these and in other regards, the invention relates to novel polynucleotides and polypeptides set forth in Table 1.

### BACKGROUND OF THE INVENTION

The Streptococci make up a medically important genera of microbes known to cause several types of disease in humans, including otitis media, pneumonia and meningitis. Since its isolation more than 100 years ago, *Streptococcus pneumoniae* (herein *S. pneumoniae*) has been one of the more intensively studied microbes. For example, much of our early understanding that DNA is, in fact, the genetic material was predicated on the work of Griffith and of Avery, Macleod and McCarty using this microbe. Despite the vast amount of research with *S. pneumoniae*, many questions concerning the virulence of this microbe remain.

While certain Streptococcal factors associated with pathogenicity have been identified, e.g., capsule polysaccharides, peptidoglycans, pneumolysins, PspA Complement factor H binding component, autolysin, neuraminidase, peptide permeases, hydrogen peroxide, IgA1 protease, the list is certainly not complete. Further very little is known concerning the temporal expression of such genes during infection and disease progression in a mammalian host. Discovering the sets of genes the bacterium is likely to be expressing at the different stages of infection, particularly when an infection is established, provides critical information for the screening and characterization of novel antibacterials which can interrupt pathogenesis. In addition to providing a fuller understanding of known proteins, such an approach will identify previously unrecognized targets.

GUG is used as an initiating nucleotide, rather than ATG, for a significant number of mRNA's in both Gram positive and Gram negative bacteria. Statistics on the frequency of NTG codons in the start codon for several bacterial species are available on line via computer at [http://biochem.otago.ac.nz:800/Transterm/home\\_page.html](http://biochem.otago.ac.nz:800/Transterm/home_page.html)).

A discussion of initiation codons in *B. subtilis* is set forth in Vellanoweth, RL.1993 in Bacillus subtilis and other Gram Positive Bacteria, Biochemistry, Physiology and Molecular Genetics, Sonenshein, Hoch, Losick Eds. Amer. Soc. Microbiol, Washington DC. p. 699-711. Vellenworth indicates a major difference between *B. subtilis* and the gram-negative organisms is in the choice of initiation codon. 91% of the sequenced *E. coli*

genes start with AUG. By contrast, about 30% of *B. subtilis* and other clostridial branch genes start with UUG or GUG. Moreover, CUG functions as a start codon in *B. subtilis*. Mutations of an AUG initiation codon to GUG or UUG often cause decreased expression in *B. subtilis* and *E. coli*. Generally, translation efficiency is higher with AUG initiation codons. A strong Shine-Delgarno ribosome binding site, however, can compensate almost fully for a weak initiation codon. It has been reported that genes with a range of expression levels have initiation codons other than ATG in gram positives (Vellanoth, RL.1993 in Bacillus subtilis and other Gram Positive Bacteria, Biochemistry, Physiology and Molecular Genetics, Sonenshein, Hoch, Losick Eds. Amer. Soc. Microbiol, Washington DC. p. 699-711).

Provided herein are ORF sequences from genes possessing GUG initiation codons and proteins expressed therefrom and homologues thereto to be used for screening for antimicrobial compounds. Clearly, there is a need for polypeptide and polynucleotide sequences that may be used to screen for antimicrobial compound and which may also be used to determine the roles of such sequences in pathogenesis of infection, dysfunction and disease. There is also need, therefore, for identification and characterization of such sequences which may play a role in preventing, ameliorating or correcting infections, dysfunctions or diseases.

The polypeptides of the invention have amino acid sequence homology to a known protein(s) as set forth in Table 1.

#### **SUMMARY OF THE INVENTION**

It is an object of the invention to provide polypeptides that have been identified as novel polypeptides by homology between an amino acid sequence selected from the group consisting of the sequences set out in Table 1 and a known amino acid sequence or sequences of other proteins such as the protein identities listed in Table 1.

It is a further object of the invention to provide polynucleotides that encode novel polypeptides, particularly polynucleotides that encode polypeptides of *Streptococcus pneumoniae*.

In a particularly preferred embodiment of the invention the polynucleotide comprises a region encoding a polypeptide comprising a sequence selected from the group consisting of the sequences set out in Table 1, or a variant of any of these sequences.

In another particularly preferred embodiment of the invention there is a novel protein from *Streptococcus pneumoniae* comprising an amino acid sequence selected from the group consisting of the sequences set out in Table 1, or a variant of any of these sequences.



In accordance with another aspect of the invention there is provided an isolated nucleic acid molecule encoding a mature polypeptide expressible by the *Streptococcus pneumoniae* 0100993 strain contained in the deposited strain.

A further aspect of the invention there are provided isolated nucleic acid molecules encoding a polypeptide of the invention, particularly *Streptococcus pneumoniae* polypeptide, and including mRNAs, cDNAs, genomic DNAs. Further embodiments of the invention include biologically, diagnostically, prophylactically, clinically or therapeutically useful variants thereof, and compositions comprising the same.

In accordance with another aspect of the invention, there is provided the use of a polynucleotide of the invention for therapeutic or prophylactic purposes, in particular genetic immunization. Among the particularly preferred embodiments of the invention are naturally occurring allelic variants of a polypeptide of the invention and polypeptides encoded thereby.

Another aspect of the invention there are provided novel polypeptides of *Streptococcus pneumoniae* as well as biologically, diagnostically, prophylactically, clinically or therapeutically useful variants thereof, and compositions comprising the same.

Among the particularly preferred embodiments of the invention are variants of the polypeptides of the invention encoded by naturally occurring alleles of their genes.

In a preferred embodiment of the invention there are provided methods for producing the aforementioned polypeptides.

In accordance with yet another aspect of the invention, there are provided inhibitors to such polypeptides, useful as antibacterial agents, including, for example, antibodies.

In accordance with certain preferred embodiments of the invention, there are provided products, compositions and methods for assessing expression of the polypeptides and polynucleotides of the invention, treating disease, for example, including, for example, otitis media, conjunctivitis, pneumonia, bacteremia, meningitis, sinusitis, pleural empyema and endocarditis, and most particularly meningitis, such as for example infection of cerebrospinal fluid, assaying genetic variation, and administering a polypeptide or polynucleotide of the invention to an organism to raise an immunological response against a bacteria, especially a *Streptococcus pneumoniae* bacteria.

In accordance with certain preferred embodiments of this and other aspects of the invention there are provided polynucleotides that hybridize to a polynucleotide sequence of the invention, particularly under stringent conditions.

In certain preferred embodiments of the invention there are provided antibodies against polypeptides of the invention.

In other embodiments of the invention there are provided methods for identifying compounds which bind to or otherwise interact with and inhibit or activate an activity of a polypeptide or polynucleotide of the invention comprising: contacting a polypeptide or polynucleotide of the invention with a compound to be screened under conditions to permit binding to or other interaction between the compound and the polypeptide or polynucleotide to assess the binding to or other interaction with the compound, such binding or interaction being associated with a second component capable of providing a detectable signal in response to the binding or interaction of the polypeptide or polynucleotide with the compound; and determining whether the compound binds to or otherwise interacts with and activates or inhibits an activity of the polypeptide or polynucleotide by detecting the presence or absence of a signal generated from the binding or interaction of the compound with the polypeptide or polynucleotide.

In accordance with yet another aspect of the invention, there are provided agonists and antagonists of the polypeptides and polynucleotides of the invention, preferably bacteriostatic or bacteriocidal agonists and antagonists.

In a further aspect of the invention there are provided compositions comprising a polynucleotide or a polypeptide of the invention for administration to a cell or to a multicellular organism.

Various changes and modifications within the spirit and scope of the disclosed invention will become readily apparent to those skilled in the art from reading the following descriptions and from reading the other parts of the present disclosure.

## **GLOSSARY**

The following definitions are provided to facilitate understanding of certain terms used frequently herein.

"Disease(s)" means any bacterial infection, but preferably a streptococcal infection, such as, otitis media, conjunctivitis, pneumonia, bacteremia, meningitis, sinusitis, pleural empyema, endocarditis, meningitis, and infection of cerebrospinal fluid.

"Host cell" is a cell which has been transformed or transfected, or is capable of transformation or transfection by an exogenous polynucleotide sequence.

"Identity," as known in the art, is a relationship between two or more polypeptide sequences or two or more polynucleotide sequences, as determined by comparing the sequences. In the art, "identity" also means the degree of sequence relatedness between polypeptide or polynucleotide sequences, as the case may be, as determined by the match between strings

of such sequences. "Identity" and "similarity" can be readily calculated by known methods, including but not limited to those described in (*Computational Molecular Biology*, Lesk, A.M., ed., Oxford University Press, New York, 1988; *Biocomputing: Informatics and Genome Projects*, Smith, D.W., ed., Academic Press, New York, 1993; *Computer Analysis of Sequence Data*, Part I, Griffin, A.M., and Griffin, H.G., eds., Humana Press, New Jersey, 1994; *Sequence Analysis in Molecular Biology*, von Heinje, G., Academic Press, 1987; and *Sequence Analysis Primer*, Gribskov, M. and Devereux, J., eds., M Stockton Press, New York, 1991; and Carillo, H., and Lipman, D., *SIAM J. Applied Math.*, 48: 1073 (1988). Preferred methods to determine identity are designed to give the largest match between the sequences tested. Methods to determine identity and similarity are codified in publicly available computer programs. Preferred computer program methods to determine identity and similarity between two sequences include, but are not limited to, the GCG program package (Devereux, J., et al., *Nucleic Acids Research* 12(1): 387 (1984)), BLASTP, BLASTN, and FASTA (Atschul, S.F. et al., *J. Molec. Biol.* 215: 403-410 (1990)). The BLAST X program is publicly available from NCBI and other sources (*BLAST Manual*, Altschul, S., et al., NCBI NLM NIH Bethesda, MD 20894; Altschul, S., et al., *J. Mol. Biol.* 215: 403-410 (1990)). As an illustration, by a polynucleotide having a nucleotide sequence having at least, for example, 95% "identity" to a reference nucleotide sequence it is intended that the nucleotide sequence of the tested polynucleotide is identical to the reference sequence except that the polynucleotide sequence may include up to five point mutations per each 100 nucleotides of the reference nucleotide sequence. In other words, to obtain a polynucleotide having a nucleotide sequence at least 95% identical to a reference nucleotide sequence, up to 5% of the nucleotides in the reference sequence may be deleted or substituted with another nucleotide, or a number of nucleotides up to 5% of the total nucleotides in the reference sequence may be inserted into the reference sequence. These mutations of the reference sequence may occur at the 5' or 3' terminal positions of the reference nucleotide sequence or anywhere between those terminal positions, interspersed either individually among nucleotides in the reference sequence or in one or more contiguous groups within the reference sequence. Analogously, by a polypeptide having an amino acid sequence having at least, for example, 95% identity to a reference amino acid sequence is intended that the test amino acid sequence of the polypeptide is identical to the reference sequence except that the polypeptide sequence may include up to five amino acid alterations per each 100 amino acids of the reference amino acid. In other words, to obtain a polypeptide having an amino acid sequence at least 95% identical to a reference amino

acid sequence, up to 5% of the amino acid residues in the reference sequence may be deleted or substituted with another amino acid, or a number of amino acids up to 5% of the total amino acid residues in the reference sequence may be inserted into the reference sequence. These alterations of the reference sequence may occur at the amino or carboxy terminal positions of the reference amino acid sequence or anywhere between those terminal positions, interspersed either individually among residues in the reference sequence or in one or more contiguous groups within the reference sequence.

"Isolated" means altered "by the hand of man" from its natural state, *i.e.*, if it occurs in nature, it has been changed or removed from its original environment, or both. For example, a polynucleotide or a polypeptide naturally present in a living organism is not "isolated," but the same polynucleotide or polypeptide separated from the coexisting materials of its natural state is "isolated", as the term is employed herein.

"Polynucleotide(s)" generally refers to any polyribonucleotide or polydeoxiribonucleotide, which may be unmodified RNA or DNA or modified RNA or DNA. "Polynucleotide(s)" include, without limitation, single- and double-stranded DNA, DNA that is a mixture of single- and double-stranded regions or single-, double- and triple-stranded regions, single- and double-stranded RNA, and RNA that is mixture of single- and double-stranded regions, hybrid molecules comprising DNA and RNA that may be single-stranded or, more typically, double-stranded, or triple-stranded regions, or a mixture of single- and double-stranded regions. In addition, "polynucleotide" as used herein refers to triple-stranded regions comprising RNA or DNA or both RNA and DNA. The strands in such regions may be from the same molecule or from different molecules. The regions may include all of one or more of the molecules, but more typically involve only a region of some of the molecules. One of the molecules of a triple-helical region often is an oligonucleotide. As used herein, the term "polynucleotide(s)" also includes DNAs or RNAs as described above that contain one or more modified bases. Thus, DNAs or RNAs with backbones modified for stability or for other reasons are "polynucleotide(s)" as that term is intended herein. Moreover, DNAs or RNAs comprising unusual bases, such as inosine, or modified bases, such as tritylated bases, to name just two examples, are polynucleotides as the term is used herein. It will be appreciated that a great variety of modifications have been made to DNA and RNA that serve many useful purposes known to those of skill in the art. The term "polynucleotide(s)" as it is employed herein embraces such chemically, enzymatically or metabolically modified forms of polynucleotides, as well as the chemical forms of DNA and RNA characteristic of viruses and cells, including, for

example, simple and complex cells. "Polynucleotide(s)" also embraces short polynucleotides often referred to as oligonucleotide(s).

"Polypeptide(s)" refers to any peptide or protein comprising two or more amino acids joined to each other by peptide bonds or modified peptide bonds. "Polypeptide(s)" refers to both short chains, commonly referred to as peptides, oligopeptides and oligomers and to longer chains generally referred to as proteins. Polypeptides may contain amino acids other than the 20 gene encoded amino acids. "Polypeptide(s)" include those modified either by natural processes, such as processing and other post-translational modifications, but also by chemical modification techniques. Such modifications are well described in basic texts and in more detailed monographs, as well as in a voluminous research literature, and they are well known to those of skill in the art. It will be appreciated that the same type of modification may be present in the same or varying degree at several sites in a given polypeptide. Also, a given polypeptide may contain many types of modifications. Modifications can occur anywhere in a polypeptide, including the peptide backbone, the amino acid side-chains, and the amino or carboxyl termini. Modifications include, for example, acetylation, acylation, ADP-ribosylation, amidation, covalent attachment of flavin, covalent attachment of a heme moiety, covalent attachment of a nucleotide or nucleotide derivative, covalent attachment of a lipid or lipid derivative, covalent attachment of phosphatidylinositol, cross-linking, cyclization, disulfide bond formation, demethylation, formation of covalent cross-links, formation of cysteine, formation of pyroglutamate, formylation, gamma-carboxylation, glycosylation, GPI anchor formation, hydroxylation, iodination, methylation, myristoylation, oxidation, proteolytic processing, phosphorylation, prenylation, racemization, glycosylation, lipid attachment, sulfation, gamma-carboxylation of glutamic acid residues, hydroxylation and ADP-ribosylation, selenoylation, sulfation, transfer-RNA mediated addition of amino acids to proteins, such as arginylation, and ubiquitination. See, for instance, *PROTEINS - STRUCTURE AND MOLECULAR PROPERTIES*, 2nd Ed., T. E. Creighton, W. H. Freeman and Company, New York (1993) and Wold, F., Posttranslational Protein Modifications: Perspectives and Prospects, pgs. 1-12 in *POSTTRANSLATIONAL COVALENT MODIFICATION OF PROTEINS*, B. C. Johnson, Ed., Academic Press, New York (1983); Seifter et al., *Meth. Enzymol.* 182:626-646 (1990) and Rattan et al., *Protein Synthesis: Posttranslational Modifications and Aging*, Ann. N.Y. Acad. Sci. 663: 48-62 (1992). Polypeptides may be branched or cyclic, with or without branching. Cyclic, branched and branched circular polypeptides may result from post-translational natural processes and may be made by entirely synthetic methods, as well.

“Variant(s)” as the term is used herein, is a polynucleotide or polypeptide that differs from a reference polynucleotide or polypeptide respectively, but retains essential properties. A typical variant of a polynucleotide differs in nucleotide sequence from another, reference polynucleotide. Changes in the nucleotide sequence of the variant may or may not alter the amino acid sequence of a polypeptide encoded by the reference polynucleotide. Nucleotide changes may result in amino acid substitutions, additions, deletions, fusions and truncations in the polypeptide encoded by the reference sequence, as discussed below. A typical variant of a polypeptide differs in amino acid sequence from another, reference polypeptide. Generally, differences are limited so that the sequences of the reference polypeptide and the variant are closely similar overall and, in many regions, identical. A variant and reference polypeptide may differ in amino acid sequence by one or more substitutions, additions, deletions in any combination. A substituted or inserted amino acid residue may or may not be one encoded by the genetic code. A variant of a polynucleotide or polypeptide may be a naturally occurring such as an allelic variant, or it may be a variant that is not known to occur naturally. Non-naturally occurring variants of polynucleotides and polypeptides may be made by mutagenesis techniques, by direct synthesis, and by other recombinant methods known to skilled artisans.

#### **DESCRIPTION OF THE INVENTION**

Each of polynucleotide and polypeptide sequences provided herein may be used in the discovery and development of antibacterial compounds. Upon expression of the sequences with the appropriate initiation and termination codons the encoded polypeptide can be used as a target for the screening of antimicrobial drugs. Additionally, the DNA sequences encoding preferably the amino terminal regions of the encoded protein or the Shine-Delgarno region can be used to construct antisense sequences to control the expression of the coding sequence of interest. Furthermore, many of the sequences disclosed herein also provide regions upstream and downstream from the encoding sequence. These sequences are useful as a source of regulatory elements for the control of bacterial gene expression. Such sequences are conveniently isolated by restriction enzyme action or synthesized chemically and introduced, for example, into promoter identification strains. These strains contain a reporter structural gene sequence located downstream from a restriction site such that if an active promoter is inserted, the reporter gene will be expressed.

Although each of the sequences may be employed as described above, this invention also provides several means for identifying particularly useful target genes. The

first of these approaches entails searching appropriate databases for sequence matches in related organisms. Thus, if a homologue exists, the Streptococcal-like form of this gene would likely play an analogous role. For example, a Streptococcal protein identified as homologous to a cell surface protein in another organism would be useful as a vaccine candidate. To the extent such homologies have been identified for the sequences disclosed herein they are reported along with the encoding sequence.

Each of the DNA sequences provided herein may be used in the discovery and development of antibacterial compounds. Because each of the sequences contains an open reading frame (ORF) with an appropriate initiation and termination codons, the encoded protein upon expression can be used as a target for the screening of antimicrobial drugs. Additionally, the DNA sequences encoding the amino terminal regions of the encoded protein can be used to construct antisense sequences to control the expression of the coding sequence of interest. Furthermore, many of the sequences disclosed herein also provide regions upstream and downstream from the encoding sequence. These sequences are useful as a source of regulatory elements for the control of bacterial gene expression. Such sequences are conveniently isolated by restriction enzyme action or synthesized chemically and introduced, for example, into promoter identification strains. These strains contain a reporter structural gene sequence located downstream from a restriction site such that if an active promoter is inserted, the reporter gene will be expressed.

It is believed that bacteria possess a number of ways of regulating gene expression levels, especially in subtle degrees, and the interplay between ribosome binding site and initiation codon is utilized for this purpose for these genes. It is also believed that such genes will be important targets for antimicrobial drug discovery, particularly since pathogenesis genes are believed undergo gene expression regulation during in the pathogenesis process. Therefore, the invention provides ORF sequences possessing a GTG (GUG ) initiation codon and protein targets expressed therefrom.

Although each of the sequences may be employed as described above, this invention also provides several means for identifying particularly useful target genes. The first of these approaches entails searching appropriate databases for sequence matches in related organisms. Thus, if a homologue exists, the Streptococcal-like form of this gene would likely play an analogous role. For example, a Streptococcal protein identified as homologous to a cell surface protein in another organism would be useful as a vaccine candidate. To the extent such homologies have been identified for the sequences disclosed herein they are reported along with the encoding sequence.

### ORF Gene Expression

Recently techniques have become available to evaluate temporal gene expression in bacteria, particularly as it applies to viability under laboratory and infection conditions. A number of methods can be used to identify genes which are essential to survival *per se*, or essential to the establishment/maintenance of an infection. Identification of an ORF unknown by one of these methods yields additional information about its function and permits the selection of such an ORF for further development as a screening target. Briefly, these approaches include:

**1) Signature Tagged Mutagenesis (STM):** This technique is described by Hensel *et al.*, Science 269: 400-403(1995), the contents of which is incorporated by reference for background purposes. Signature tagged mutagenesis identifies genes necessary for the establishment/maintenance of infection in a given infection model.

The basis of the technique is the random mutagenesis of target organism by various means (e.g., transposons) such that unique DNA sequence tags are inserted in close proximity to the site of mutation. The tags from a mixed population of bacterial mutants and bacteria recovered from an infected hosts are detected by amplification, radiolabeling and hybridisation analysis. Mutants attenuated in virulence are revealed by absence of the tag from the pool of bacteria recovered from infected hosts.

In *Streptococcus pneumoniae*, because the transposon system is less well developed, a more efficient way of creating the tagged mutants is to use the insertion-duplication mutagenesis technique as described by Morrison *et al.*, J. Bacteriol. 159:870 (1984) the contents of which is incorporated by reference for background purposes.

**2) In Vivo Expression Technology (IVET):** This technique is described by Camilli *et al.*, Proc. Nat'l. Acad. Sci. USA. 91:2634-2638 (1994), the contents of which is incorporated by reference for background purposes. IVET identifies genes up-regulated during infection when compared to laboratory cultivation, implying an important role in infection. ORF identified by this technique are implied to have a significant role in infection establishment/maintenance.

In this technique random chromosomal fragments of target organism are cloned upstream of a promoter-less recombinase gene in a plasmid vector. This construct is introduced into the target organism which carries an antibiotic resistance gene flanked by resolvase sites. Growth in the presence of the antibiotic removes from the population those fragments cloned into the plasmid vector capable of supporting transcription of the recombinase gene and therefore have caused loss of antibiotic resistance. The resistant pool



is introduced into a host and at various times after infection bacteria may be recovered and assessed for the presence of antibiotic resistance. The chromosomal fragment carried by each antibiotic sensitive bacterium should carry a promoter or portion of a gene normally upregulated during infection. Sequencing upstream of the recombinase gene allows identification of the up regulated gene.

**3) Differential display:** This technique is described by Chuang *et al.*, *J. Bacteriol.* 175:2026-2036 (1993), the contents of which is incorporated by reference for background purposes. This method identifies those genes which are expressed in an organism by identifying mRNA present using randomly-primed RT-PCR. By comparing pre-infection and post infection profiles, genes up and down regulated during infection can be identified and the RT-PCR product sequenced and matched to ORF 'unknowns'.

**4) Generation of conditional lethal mutants by transposon mutagenesis:** This technique, described by de Lorenzo, V. *et al.*, *Gene* 123:17-24 (1993); Neuwald, A. F. *et al.*, *Gene* 125: 69-73(1993); and Takiff, H. E. *et al.*, *J. Bacteriol.* 174:1544-1553(1992), the contents of which is incorporated by reference for background purposes, identifies genes whose expression are essential for cell viability.

In this technique transposons carrying controllable promoters, which provide transcription outward from the transposon in one or both directions, are generated. Random insertion of these transposons into target organisms and subsequent isolation of insertion mutants in the presence of inducer of promoter activity ensures that insertions which separate promoter from coding region of a gene whose expression is essential for cell viability will be recovered. Subsequent replica plating in the absence of inducer identifies such insertions, since they fail to survive. Sequencing of the flanking regions of the transposon allows identification of site of insertion and identification of the gene disrupted. Close monitoring of the changes in cellular processes/morphology during growth in the absence of inducer yields information on likely function of the gene. Such monitoring could include flow cytometry (cell division, lysis, redox potential, DNA replication), incorporation of radiochemically labeled precursors into DNA, RNA, protein, lipid, peptidoglycan, monitoring reporter enzyme gene fusions which respond to known cellular stresses.

**5) Generation of conditional lethal mutants by chemical mutagenesis:** This technique is described by Beckwith, J., *Methods in Enzymology* 204: 3-18(1991), the contents of which are incorporated herein by reference for background purposes. In this technique random chemical mutagenesis of target organism, growth at

temperature other than physiological temperature (permissive temperature) and subsequent replica plating and growth at different temperature (e.g. 42°C to identify ts, 25°C to identify cs) are used to identify those isolates which now fail to grow (conditional mutants). As above close monitoring of the changes upon growth at the non-permissive temperature yields information on the function of the mutated gene. Complementation of conditional lethal mutation by library from target organism and sequencing of complementing gene allows matching with unknown ORF.

**6) RT-PCR:** *Streptococcus pneumoniae* messenger RNA is isolated from bacterial infected tissue e.g. 48 hour murine lung infections, and the amount of each mRNA species assessed by reverse transcription of the RNA sample primed with random hexanucleotides followed by PCR with gene specific primer pairs. The determination of the presence and amount of a particular mRNA species by quantification of the resultant PCR product provides information on the bacterial genes which are transcribed in the infected tissue. Analysis of gene transcription can be carried out at different times of infection to gain a detailed knowledge of gene regulation in bacterial pathogenesis allowing for a clearer understanding of which gene products represent targets for screens for novel antibacterials. Because of the gene specific nature of the PCR primers employed it should be understood that the bacterial mRNA preparation need not be free of mammalian RNA. This allows the investigator to carry out a simple and quick RNA preparation from infected tissue to obtain bacterial mRNA species which are very short lived in the bacterium (in the order of 2 minute halflives). Optimally the bacterial mRNA is prepared from infected murine lung tissue by mechanical disruption in the presence of TRIzol (GIBCO-BRL) for very short periods of time, subsequent processing according to the manufacturers of TRIzol reagent and DNAase treatment to remove contaminating DNA. Preferably the process is optimised by finding those conditions which give a maximum amount of *Streptococcus pneumoniae* 16S ribosomal RNA as detected by probing Northern blots with a suitably labelled sequence specific oligonucleotide probe. Typically a 5' dye labelled primer is used in each PCR primer pair in a PCR reaction which is terminated optimally between 8 and 25 cycles. The PCR products are separated on 6% polyacrylamide gels with detection and quantification using GeneScanner (manufactured by ABI).

Each of these techniques may have advantages or disadvantage depending on the particular application. The skilled artisan would choose the approach that is the most relevant with the particular end use in mind.

Use of the of these technologies when applied to the ORFs of the present invention enables identification of bacterial proteins expressed during infection, inhibitors of which would have utility in anti-bacterial therapy.

The invention relates to novel polypeptides and polynucleotides as described in greater detail below. In particular, the invention relates to polypeptides and polynucleotides of *Streptococcus pneumoniae*, which is related by amino acid sequence homology to known polypeptide as set forth in Table 1. The invention relates especially to compounds having the nucleotide and amino acid sequence selected from the group consisting of the sequences set out in Table 1, and to the nucleotide sequences of the DNA in the deposited strain and amino acid sequences encoded thereby.

#### **Deposited materials**

The deposit has been made under the terms of the Budapest Treaty on the International Recognition of the Deposit of Micro-organisms for Purposes of Patent Procedure. The strain will be irrevocably and without restriction or condition released to the public upon the issuance of a patent. The deposit is provided merely as convenience to those of skill in the art and is not an admission that a deposit is required for enablement, such as that required under 35 U.S.C. §112.

A deposit containing a *Streptococcus pneumoniae* bacterial strain has been deposited with the National Collections of Industrial and Marine Bacteria Ltd. (NCIMB), 23 St. Machar Drive, Aberdeen AB2 1RY, Scotland on 11 April 1996 and assigned NCIMB Deposit No. 40794. The *Streptococcus pneumoniae* bacterial strain deposit is referred to herein as "the deposited bacterial strain" or as "the DNA of the deposited bacterial strain."

The deposited material is a bacterial strain that contains the full length FabH DNA, referred to as "NCIMB 40794" upon deposit.

The sequence of the polynucleotides contained in the deposited material, as well as the amino acid sequence of the polypeptide encoded thereby, are controlling in the event of any conflict with any description of sequences herein.

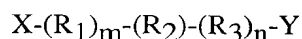
A license may be required to make, use or sell the deposited materials, and no such license is hereby granted.

The deposited strain contains the full length genes comprising the polynucleotides set forth in Table 1. The sequence of the polynucleotides contained in the deposited strain, as well as the amino acid sequence of the polypeptide encoded thereby, are controlling in the event of any conflict with any description of sequences herein.

#### **Polypeptides**

The polypeptides of the invention include the polypeptides set forth in Table 1 (in particular the mature polypeptide) as well as polypeptides and fragments, particularly those which have the biological activity of a polypeptide of the invention, and also those which have at least 50%, 60% or 70% identity to a polypeptide sequence selected from the group consisting of the sequences set out in Table 1 or the relevant portion, preferably at least 80% identity to a polypeptide sequence selected from the group consisting of the sequences set out in Table 1, and more preferably at least 90% similarity (more preferably at least 90% identity) to a polypeptide sequence selected from the group consisting of the sequences set out in Table 1, and still more preferably at least 95% similarity (still more preferably at least 95% identity) to a polypeptide sequence selected from the group consisting of the sequences set out in Table 1, and also include portions of such polypeptides with such portion of the polypeptide generally containing at least 30 amino acids and more preferably at least 50 amino acids.

The invention also includes polypeptides of the formula:



wherein, at the amino terminus, X is hydrogen, and at the carboxyl terminus, Y is hydrogen or a metal,  $R_1$  and  $R_3$  are any amino acid residue, n is an integer between 1 and 2000, m is an integer between 1 and 2000, and  $R_2$  is an amino acid sequence of the invention, particularly an amino acid sequence selected from the group set forth in Table 1. In the formula above  $R_2$  is oriented so that its amino terminal residue is at the left, bound to  $R_1$ , and its carboxy terminal residue is at the right, bound to  $R_3$ . Any stretch of amino acid residues denoted by either R group, where R is greater than 1, may be either a heteropolymer or a homopolymer, preferably a heteropolymer. In preferred embodiments n is an integer between 1 and 1000 or 2000.

A fragment is a variant polypeptide having an amino acid sequence that entirely is the same as part but not all of the amino acid sequence of the aforementioned polypeptides. As with polypeptides, fragments may be "free-standing," or comprised within a larger polypeptide of which they form a part or region, most preferably as a single continuous region, a single larger polypeptide.

Preferred fragments include, for example, truncation polypeptides having a portion of the amino acid sequence of Table 1, or of variants thereof, such as a continuous series of residues that includes the amino terminus, or a continuous series of residues that includes the carboxyl terminus. Degradation forms of the polypeptides of the invention in a host cell, particularly a *Streptococcus pneumoniae*, are also preferred. Further preferred are fragments characterized by structural or functional attributes such as fragments that comprise alpha-helix and alpha-helix forming regions, beta-sheet and beta-sheet-forming regions, turn and turn-forming regions, coil

and coil-forming regions, hydrophilic regions, hydrophobic regions, alpha amphipathic regions, beta amphipathic regions, flexible regions, surface-forming regions, substrate binding region, and high antigenic index regions.

Also preferred are biologically active fragments which are those fragments that mediate activities of polypeptides of the invention, including those with a similar activity or an improved activity, or with a decreased undesirable activity. Also included are those fragments that are antigenic or immunogenic in an animal, especially in a human. Particularly preferred are fragments comprising receptors or domains of enzymes that confer a function essential for viability of *Streptococcus pneumoniae* or the ability to initiate, or maintain cause disease in an individual, particularly a human.

Variants that are fragments of the polypeptides of the invention may be employed for producing the corresponding full-length polypeptide by peptide synthesis; therefore, these variants may be employed as intermediates for producing the full-length polypeptides of the invention.

In addition to the standard single and triple letter representations for amino acids, the term "X" or "Xaa" is also used. "X" and "Xaa" mean that any of the twenty naturally occurring amino acids may appear at such a designated position in the polypeptide sequence.

#### **Polynucleotides**

The nucleotide sequences disclosed herein can be obtained by synthetic chemical techniques known in the art or can be obtained from *S. pneumoniae* 0100993 by probing a DNA preparation with probes constructed from the particular sequences disclosed herein. Alternatively, oligonucleotides derived from a disclosed sequence can act as PCR primers in a process of PCR-based cloning of the sequence from a bacterial genomic source. It is recognised that such sequences will also have utility in diagnosis of the stage of infection and type of infection the pathogen has attained.

To obtain the polynucleotide encoding the protein using the DNA sequence given herein typically a library of clones of chromosomal DNA of *S.pneumoniae* 0100993 in *E. coli* or some other suitable host is probed with a radiolabelled oligonucleotide, preferably a 17mer or longer, derived from the partial sequence. Clones carrying DNA identical to that of the probe can then be distinguished using high stringency washes. By sequencing the individual clones thus identified with sequencing primers designed from the original sequence it is then possible to extend the sequence in both directions to determine the full gene sequence. Conveniently such sequencing is performed using denatured double stranded DNA prepared from a plasmid clone. Suitable techniques are described by

Maniatis, T., Fritsch, E.F. and Sambrook, J. in *MOLECULAR CLONING, A Laboratory Manual*, 2nd edition, 1989, Cold Spring Harbor Laboratory (see: Screening By Hybridization 1.90 and Sequencing Denatured Double-Stranded DNA Templates 13.70).

Moreover, another aspect of the invention relates to isolated polynucleotides that encode the polypeptides of the invention having a deduced amino acid sequence selected from the group consisting of the sequences in Table 1 and polynucleotides closely related thereto and variants thereof.

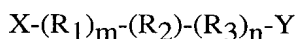
Using the information provided herein, such as the polynucleotide sequences set out in Table 1, a polynucleotide of the invention encoding polypeptide may be obtained using standard cloning and screening methods, such as those for cloning and sequencing chromosomal DNA fragments from bacteria using *Streptococcus pneumoniae* 0100993 cells as starting material, followed by obtaining a full length clone. For example, to obtain a polynucleotide sequence of the invention, such as a sequence set forth in Table 1, typically a library of clones of chromosomal DNA of *Streptococcus pneumoniae* 0100993 in *E.coli* or some other suitable host is probed with a radiolabeled oligonucleotide, preferably a 17-mer or longer, derived from a partial sequence. Clones carrying DNA identical to that of the probe can then be distinguished using stringent conditions. By sequencing the individual clones thus identified with sequencing primers designed from the original sequence it is then possible to extend the sequence in both directions to determine the full gene sequence. Conveniently, such sequencing is performed using denatured double stranded DNA prepared from a plasmid clone. Suitable techniques are described by Maniatis, T., Fritsch, E.F. and Sambrook et al., *MOLECULAR CLONING, A LABORATORY MANUAL*, 2nd Ed.; Cold Spring Harbor Laboratory Press, Cold Spring Harbor, New York (1989). (see in particular Screening By Hybridization 1.90 and Sequencing Denatured Double-Stranded DNA Templates 13.70). Illustrative of the invention, the polynucleotides set out in Table 1 were discovered in a DNA library derived from *Streptococcus pneumoniae* 0100993.

The DNA sequences set out in Table 1 each contains at least one open reading frame encoding a protein having at least about the number of amino acid residues set forth in Table 1. The start and stop codons of each open reading frame (herein "ORF") DNA are the first three and the last three nucleotides of each polynucleotide set forth in Table 1.

Certain polynucleotides and polypeptides of the invention are structurally related to known proteins as set forth in Table 1. These proteins exhibit greatest homology to the homologue listed in Table 1 from among the known proteins.

The invention provides a polynucleotide sequence identical over its entire length to each coding sequence in Table 1. Also provided by the invention is the coding sequence for the mature polypeptide or a fragment thereof, by itself as well as the coding sequence for the mature polypeptide or a fragment in reading frame with other coding sequence, such as those encoding a leader or secretory sequence, a pre-, or pro- or prepro- protein sequence. The polynucleotide may also contain non-coding sequences, including for example, but not limited to non-coding 5' and 3' sequences, such as the transcribed, non-translated sequences, termination signals, ribosome binding sites, sequences that stabilize mRNA, introns, polyadenylation signals, and additional coding sequence which encode additional amino acids. For example, a marker sequence that facilitates purification of the fused polypeptide can be encoded. In certain embodiments of the invention, the marker sequence is a hexa-histidine peptide, as provided in the pQE vector (Qiagen, Inc.) and described in Gentz *et al.*, *Proc. Natl. Acad. Sci., USA* 86: 821-824 (1989), or an HA tag (Wilson *et al.*, *Cell* 37: 767 (1984). Polynucleotides of the invention also include, but are not limited to, polynucleotides comprising a structural gene and its naturally associated sequences that control gene expression.

The invention also includes polynucleotides of the formula:



wherein, at the 5' end of the molecule, X is hydrogen, and at the 3' end of the molecule, Y is hydrogen or a metal,  $R_1$  and  $R_3$  is any nucleic acid residue, n is an integer between 1 and 3000, m is an integer between 1 and 3000, and  $R_2$  is a nucleic acid sequence of the invention, particularly a nucleic acid sequence selected from the group set forth in Table 1. In the polynucleotide formula above  $R_2$  is oriented so that its 5' end residue is at the left, bound to  $R_1$ , and its 3' end residue is at the right, bound to  $R_3$ . Any stretch of nucleic acid residues denoted by either R group, where R is greater than 1, may be either a heteropolymer or a homopolymer, preferably a heteropolymer. In a preferred embodiment n is an integer between 1 and 1000, or 2000 or 3000.

The term "polynucleotide encoding a polypeptide" as used herein encompasses polynucleotides that include a sequence encoding a polypeptide of the invention, particularly a bacterial polypeptide and more particularly a polypeptide of the *Streptococcus pneumoniae* having an amino acid sequence set out in Table 1. The term also encompasses polynucleotides that include a single continuous region or discontinuous regions encoding the polypeptide (for example, interrupted by integrated phage or an insertion sequence or editing) together with additional regions, that also may contain coding and/or non-coding sequences.

The invention further relates to variants of the polynucleotides described herein that encode for variants of the polypeptide having the deduced amino acid sequence of Table 1. Variants that are fragments of the polynucleotides of the invention may be used to synthesize full-length polynucleotides of the invention.

Further particularly preferred embodiments are polynucleotides encoding polypeptide variants, that have the amino acid sequence of a polypeptide of Table 1 in which several, a few, 5 to 10, 1 to 5, 1 to 3, 2, 1 or no amino acid residues are substituted, deleted or added, in any combination. Especially preferred among these are silent substitutions, additions and deletions, that do not alter the properties and activities of such polynucleotide.

Further preferred embodiments of the invention are polynucleotides that are at least 50%, 60% or 70% identical over their entire length to a polynucleotide encoding a polypeptide having the amino acid sequence set out in Table 1, and polynucleotides that are complementary to such polynucleotides. Alternatively, most highly preferred are polynucleotides that comprise a region that is at least 80% identical over its entire length to a polynucleotide encoding a polypeptide of the deposited strain and polynucleotides complementary thereto. In this regard, polynucleotides at least 90% identical over their entire length to the same are particularly preferred, and among these particularly preferred polynucleotides, those with at least 95% are especially preferred. Furthermore, those with at least 97% are highly preferred among those with at least 95%, and among these those with at least 98% and at least 99% are particularly highly preferred, with at least 99% being the more preferred.

A preferred embodiment is an isolated polynucleotide comprising a polynucleotide sequence selected from the group consisting of: a polynucleotide having at least a 50% identity to a polynucleotide encoding a polypeptide comprising the amino acid sequence of Table 1 and obtained from a prokaryotic species other than *S. pneumoniae*; and a polynucleotide encoding a polypeptide comprising an amino acid sequence which is at least 50% identical to the amino acid sequence of Table 1 and obtained from a prokaryotic species other than *S. pneumoniae*.

Preferred embodiments are polynucleotides that encode polypeptides that retain substantially the same biological function or activity as the mature polypeptide encoded by the DNA of Table 1.

The invention further relates to polynucleotides that hybridize to the herein above-described sequences. In this regard, the invention especially relates to polynucleotides that hybridize under stringent conditions to the herein above-described polynucleotides. As herein used, the terms "stringent conditions" and "stringent hybridization conditions" mean hybridization will occur only if there is at least 95% and preferably at least 97% identity between



the sequences. An example of stringent hybridization conditions is overnight incubation at 42°C in a solution comprising: 50% formamide, 5x SSC (150mM NaCl, 15mM trisodium citrate), 50 mM sodium phosphate (pH7.6), 5x Denhardt's solution, 10% dextran sulfate, and 20 micrograms/ml denatured, sheared salmon sperm DNA, followed by washing the hybridization support in 0.1x SSC at about 65°C. Hybridization and wash conditions are well known and exemplified in Sambrook, *et al.*, Molecular Cloning: A Laboratory Manual, Second Edition, Cold Spring Harbor, N.Y., (1989), particularly Chapter 11 therein.

The invention also provides a polynucleotide consisting essentially of a polynucleotide sequence obtainable by screening an appropriate library containing the complete gene for a polynucleotide sequence set forth in Table 1 under stringent hybridization conditions with a probe having the sequence of said polynucleotide sequence or a fragment thereof; and isolating said DNA sequence. Fragments useful for obtaining such a polynucleotide include, for example, probes and primers described elsewhere herein.

As discussed additionally herein regarding polynucleotide assays of the invention, for instance, polynucleotides of the invention as discussed above, may be used as a hybridization probe for RNA, cDNA and genomic DNA to isolate full-length cDNAs and genomic clones encoding a polypeptide and to isolate cDNA and genomic clones of other genes that have a high sequence similarity to a polynucleotide set forth in Table 1. Such probes generally will comprise at least 15 bases. Preferably, such probes will have at least 30 bases and may have at least 50 bases. Particularly preferred probes will have at least 30 bases and will have 50 bases or less.

For example, the coding region of each gene that comprises or is comprised by a polynucleotide set forth in Table 1 may be isolated by screening using a DNA sequence provided in Table 1 to synthesize an oligonucleotide probe. A labeled oligonucleotide having a sequence complementary to that of a gene of the invention is then used to screen a library of cDNA, genomic DNA or mRNA to determine which members of the library the probe hybridizes to.

The polynucleotides and polypeptides of the invention may be employed, for example, as research reagents and materials for discovery of treatments of and diagnostics for disease, particularly human disease, as further discussed herein relating to polynucleotide assays.

Polynucleotides of the invention that are oligonucleotides derived from the a polynucleotide or polypeptide sequence set forth in Table 1 may be used in the processes herein as described, but preferably for PCR, to determine whether or not the polynucleotides identified herein in whole or in part are transcribed in bacteria in infected tissue. It is recognized that such sequences will also have utility in diagnosis of the stage of infection and type of infection the pathogen has attained.

The invention also provides polynucleotides that may encode a polypeptide that is the mature protein plus additional amino or carboxyl-terminal amino acids, or amino acids interior to the mature polypeptide (when the mature form has more than one polypeptide chain, for instance). Such sequences may play a role in processing of a protein from precursor to a mature form, may allow protein transport, may lengthen or shorten protein half-life or may facilitate manipulation of a protein for assay or production, among other things. As generally is the case *in vivo*, the additional amino acids may be processed away from the mature protein by cellular enzymes.

A precursor protein, having the mature form of the polypeptide fused to one or more prosequences may be an inactive form of the polypeptide. When prosequences are removed such inactive precursors generally are activated. Some or all of the prosequences may be removed before activation. Generally, such precursors are called proproteins.

In addition to the standard A, G, C, T/U representations for nucleic acid bases, the term "N" is also used. "N" means that any of the four DNA or RNA bases may appear at such a designated position in the DNA or RNA sequence, except it is preferred that N is not a base that when taken in combination with adjacent nucleotide positions, when read in the correct reading frame, would have the effect of generating a premature termination codon in such reading frame.

In sum, a polynucleotide of the invention may encode a mature protein, a mature protein plus a leader sequence (which may be referred to as a preprotein), a precursor of a mature protein having one or more prosequences that are not the leader sequences of a preprotein, or a preproprotein, which is a precursor to a proprotein, having a leader sequence and one or more prosequences, which generally are removed during processing steps that produce active and mature forms of the polypeptide.

#### **Vectors, host cells, expression**

The invention also relates to vectors that comprise a polynucleotide or polynucleotides of the invention, host cells that are genetically engineered with vectors of the invention and the production of polypeptides of the invention by recombinant techniques. Cell-free translation systems can also be employed to produce such proteins using RNAs derived from the DNA constructs of the invention.

For recombinant production, host cells can be genetically engineered to incorporate expression systems or portions thereof or polynucleotides of the invention. Introduction of a polynucleotide into the host cell can be effected by methods described in many standard laboratory manuals, such as Davis et al., *BASIC METHODS IN MOLECULAR BIOLOGY*,

(1986) and Sambrook et al., *MOLECULAR CLONING: A LABORATORY MANUAL*, 2nd Ed., Cold Spring Harbor Laboratory Press, Cold Spring Harbor, N.Y. (1989), such as, calcium phosphate transfection, DEAE-dextran mediated transfection, transvection, microinjection, cationic lipid-mediated transfection, electroporation, transduction, scrape loading, ballistic introduction and infection.

Representative examples of appropriate hosts include bacterial cells, such as streptococci, staphylococci, enterococci *E. coli*, streptomyces and *Bacillus subtilis* cells; fungal cells, such as yeast cells and *Aspergillus* cells; insect cells such as *Drosophila* S2 and *Spodoptera* Sf9 cells; animal cells such as CHO, COS, HeLa, C127, 3T3, BHK, 293 and Bowes melanoma cells; and plant cells.

A great variety of expression systems can be used to produce the polypeptides of the invention. Such vectors include, among others, chromosomal, episomal and virus-derived vectors, *e.g.*, vectors derived from bacterial plasmids, from bacteriophage, from transposons, from yeast episomes, from insertion elements, from yeast chromosomal elements, from viruses such as baculoviruses, papova viruses, such as SV40, vaccinia viruses, adenoviruses, fowl pox viruses, pseudorabies viruses and retroviruses, and vectors derived from combinations thereof, such as those derived from plasmid and bacteriophage genetic elements, such as cosmids and phagemids. The expression system constructs may contain control regions that regulate as well as engender expression. Generally, any system or vector suitable to maintain, propagate or express polynucleotides and/or to express a polypeptide in a host may be used for expression in this regard. The appropriate DNA sequence may be inserted into the expression system by any of a variety of well-known and routine techniques, such as, for example, those set forth in Sambrook *et al.*, *MOLECULAR CLONING, A LABORATORY MANUAL*, (*supra*).

For secretion of the translated protein into the lumen of the endoplasmic reticulum, into the periplasmic space or into the extracellular environment, appropriate secretion signals may be incorporated into the expressed polypeptide. These signals may be endogenous to the polypeptide or they may be heterologous signals.

Polypeptides of the invention can be recovered and purified from recombinant cell cultures by well-known methods including ammonium sulfate or ethanol precipitation, acid extraction, anion or cation exchange chromatography, phosphocellulose chromatography, hydrophobic interaction chromatography, affinity chromatography, hydroxylapatite chromatography, and lectin chromatography. Most preferably, high performance liquid chromatography is employed for purification. Well known techniques for refolding protein may

be employed to regenerate active conformation when the polypeptide is denatured during isolation and or purification.

### **Diagnostic Assays**

This invention is also related to the use of the polynucleotides of the invention for use as diagnostic reagents. Detection of such polynucleotides in a eukaryote, particularly a mammal, and especially a human, will provide a diagnostic method for diagnosis of a disease. Eukaryotes (herein also "individual(s)"), particularly mammals, and especially humans, infected with an organism comprising a gene of the invention may be detected at the nucleic acid level by a variety of techniques.

Nucleic acids for diagnosis may be obtained from an infected individual's cells and tissues, such as bone, blood, muscle, cartilage, and skin. Genomic DNA may be used directly for detection or may be amplified enzymatically by using PCR or other amplification technique prior to analysis. RNA or cDNA may also be used in the same ways. Using amplification, characterization of the species and strain of prokaryote present in an individual, may be made by an analysis of the genotype of the prokaryote gene. Deletions and insertions can be detected by a change in size of the amplified product in comparison to the genotype of a reference sequence. Point mutations can be identified by hybridizing amplified DNA to labeled polynucleotide sequences of the invention. Perfectly matched sequences can be distinguished from mismatched duplexes by RNase digestion or by differences in melting temperatures. DNA sequence differences may also be detected by alterations in the electrophoretic mobility of the DNA fragments in gels, with or without denaturing agents, or by direct DNA sequencing. See, *e.g.*, Myers et al., *Science*, 230: 1242 (1985). Sequence changes at specific locations also may be revealed by nuclease protection assays, such as RNase and S1 protection or a chemical cleavage method. See, *e.g.*, Cotton et al., *Proc. Natl. Acad. Sci., USA*, 85: 4397-4401 (1985).

Cells carrying mutations or polymorphisms in the gene of the invention may also be detected at the DNA level by a variety of techniques, to allow for serotyping, for example. For example, RT-PCR can be used to detect mutations. It is particularly preferred to use RT-PCR in conjunction with automated detection systems, such as, for example, GeneScan. RNA or cDNA may also be used for the same purpose, PCR or RT-PCR. As an example, PCR primers complementary to a nucleic acid encoding a polypeptide of the invention can be used to identify and analyze mutations. These primers may be used for, among other things, amplifying a DNA of the invention isolated from a sample derived from an individual. The primers may be used to amplify the gene isolated from an infected individual such that the gene may then be subject to

various techniques for elucidation of the DNA sequence. In this way, mutations in the DNA sequence may be detected and used to diagnose infection and to serotype and/or classify the infectious agent.

The invention further provides a process for diagnosing disease, preferably bacterial infections, more preferably infections by *Streptococcus pneumoniae*, and most preferably disease, comprising determining from a sample derived from an individual a increased level of expression of polynucleotide having the sequence of Table 1. Increased or decreased expression of a polynucleotide of the invention can be measured using any on of the methods well known in the art for the quantitation of polynucleotides, such as, for example, amplification, PCR, RT-PCR, RNase protection, Northern blotting and other hybridization methods.

In addition, a diagnostic assay in accordance with the invention for detecting over-expression of a polypeptide of the invention compared to normal control tissue samples may be used to detect the presence of an infection, for example. Assay techniques that can be used to determine levels of a protein, in a sample derived from a host are well-known to those of skill in the art. Such assay methods include radioimmunoassays, competitive-binding assays, Western Blot analysis and ELISA assays.

#### **Antibodies**

The polypeptides of the invention or variants thereof, or cells expressing them can be used as an immunogen to produce antibodies immunospecific for such polypeptides. "Antibodies" as used herein includes monoclonal and polyclonal antibodies, chimeric, single chain, simianized antibodies and humanized antibodies, as well as Fab fragments, including the products of an Fab immunoglobulin expression library.

Antibodies generated against the polypeptides of the invention can be obtained by administering the polypeptides or epitope-bearing fragments, analogues or cells to an animal, preferably a nonhuman, using routine protocols. For preparation of monoclonal antibodies, any technique known in the art that provides antibodies produced by continuous cell line cultures can be used. Examples include various techniques, such as those in Kohler, G. and Milstein, C., *Nature* 256: 495-497 (1975); Kozbor *et al.*, *Immunology Today* 4: 72 (1983); Cole *et al.*, pg. 77-96 in *MONOCLONAL ANTIBODIES AND CANCER THERAPY*, Alan R. Liss, Inc. (1985).

Techniques for the production of single chain antibodies (U.S. Patent No. 4,946,778) can be adapted to produce single chain antibodies to polypeptides of this invention. Also, transgenic mice, or other organisms such as other mammals, may be used to express humanized antibodies.

Alternatively phage display technology may be utilized to select antibody genes with binding activities towards the polypeptide either from repertoires of PCR amplified v-genes of lymphocytes from humans screened for possessing recognition of a polypeptide of the invention or from naive libraries (McCafferty, J. et al., (1990), *Nature* **348**, 552-554; Marks, J. et al., (1992) *Biotechnology* *10*, 779-783). The affinity of these antibodies can also be improved by chain shuffling (Clackson, T. et al., (1991) *Nature* **352**, 624-628).

If two antigen binding domains are present each domain may be directed against a different epitope - termed 'bispecific' antibodies.

The above-described antibodies may be employed to isolate or to identify clones expressing the polypeptides to purify the polypeptides by affinity chromatography.

Thus, among others, antibodies against a polypeptide of the invention may be employed to treat disease.

Polypeptide variants include antigenically, epitopically or immunologically equivalent variants that form a particular aspect of this invention. The term "antigenically equivalent derivative" as used herein encompasses a polypeptide or its equivalent which will be specifically recognized by certain antibodies which, when raised to the protein or polypeptide according to the invention, interfere with the immediate physical interaction between pathogen and mammalian host. The term "immunologically equivalent derivative" as used herein encompasses a peptide or its equivalent which when used in a suitable formulation to raise antibodies in a vertebrate, the antibodies act to interfere with the immediate physical interaction between pathogen and mammalian host.

The polypeptide, such as an antigenically or immunologically equivalent derivative or a fusion protein thereof is used as an antigen to immunize a mouse or other animal such as a rat or chicken. The fusion protein may provide stability to the polypeptide. The antigen may be associated, for example by conjugation, with an immunogenic carrier protein for example bovine serum albumin (BSA) or keyhole limpet haemocyanin (KLH). Alternatively a multiple antigenic peptide comprising multiple copies of the protein or polypeptide, or an antigenically or immunologically equivalent polypeptide thereof may be sufficiently antigenic to improve immunogenicity so as to obviate the use of a carrier.

Preferably, the antibody or variant thereof is modified to make it less immunogenic in the individual. For example, if the individual is human the antibody may most preferably be "humanized"; where the complementarity determining region(s) of the hybridoma-derived antibody has been transplanted into a human monoclonal antibody, for

example as described in Jones, P. et al. (1986), *Nature* 321, 522-525 or Tempest et al., (1991) *Biotechnology* 9, 266-273.

The use of a polynucleotide of the invention in genetic immunization will preferably employ a suitable delivery method such as direct injection of plasmid DNA into muscles (Wolff et al., *Hum Mol Genet* 1992, 1:363, Manthorpe et al., *Hum. Gene Ther.* 1993:4, 419), delivery of DNA complexed with specific protein carriers (Wu et al., *J Biol Chem.* 1989: 264,16985), coprecipitation of DNA with calcium phosphate (Benvenisty & Reshef, *PNAS*, 1986:83,9551), encapsulation of DNA in various forms of liposomes (Kaneda et al., *Science* 1989:243,375), particle bombardment (Tang et al., *Nature* 1992, 356:152, Eisenbraun et al., *DNA Cell Biol* 1993, 12:791) and *in vivo* infection using cloned retroviral vectors (Seeger et al., *PNAS* 1984:81,5849).

#### **Antagonists and agonists - assays and molecules**

Polypeptides of the invention may also be used to assess the binding of small molecule substrates and ligands in, for example, cells, cell-free preparations, chemical libraries, and natural product mixtures. These substrates and ligands may be natural substrates and ligands or may be structural or functional mimetics. See, *e.g.*, Coligan *et al.*, *Current Protocols in Immunology* 1(2): Chapter 5 (1991).

The invention also provides a method of screening compounds to identify those which enhance (agonist) or block (antagonist) the action of a polypeptides or polynucleotides of the invention, particularly those compounds that are bacteriostatic and/or bacteriocidal. The method of screening may involve high-throughput techniques. For example, to screen for agonists or antagonists, a synthetic reaction mix, a cellular compartment, such as a membrane, cell envelope or cell wall, or a preparation of any thereof, comprising a polypeptide of the invention and a labeled substrate or ligand of such polypeptide is incubated in the absence or the presence of a candidate molecule that may be an agonist or antagonist of a polypeptide of the invention. The ability of the candidate molecule to agonize or antagonize a polypeptide of the invention is reflected in decreased binding of the labeled ligand or decreased production of product from such substrate. Molecules that bind gratuitously, *i.e.*, without inducing the effects of a polypeptide of the invention are most likely to be good antagonists. Molecules that bind well and increase the rate of product production from substrate are agonists. Detection of the rate or level of production of product from substrate may be enhanced by using a reporter system. Reporter systems that may be useful in this regard include but are not limited to colorimetric labeled substrate converted into product, a reporter gene that is responsive to changes in polynucleotide or polypeptide activity, and binding assays known in the art.

Another example of an assay for antagonists of polypeptides of the invention is a competitive assay that combines any such polypeptide and a potential antagonist with a compound which binds such polypeptide, natural substrates or ligands, or substrate or ligand mimetics, under appropriate conditions for a competitive inhibition assay. A polypeptide of the invention can be labeled, such as by radioactivity or a colorimetric compound, such that the number of such polypeptide molecules bound to a binding molecule or converted to product can be determined accurately to assess the effectiveness of the potential antagonist.

Potential antagonists include small organic molecules, peptides, polypeptides and antibodies that bind to a polynucleotide or polypeptide of the invention and thereby inhibit or extinguish its activity. Potential antagonists also may be small organic molecules, a peptide, a polypeptide such as a closely related protein or antibody that binds the same sites on a binding molecule, such as a binding molecule, without inducing activities induced by a polypeptide of the invention, thereby preventing the action of such polypeptide by excluding it from binding.

Potential antagonists include a small molecule that binds to and occupies the binding site of the polypeptide thereby preventing binding to cellular binding molecules, such that normal biological activity is prevented. Examples of small molecules include but are not limited to small organic molecules, peptides or peptide-like molecules. Other potential antagonists include antisense molecules (see Okano, *J. Neurochem.* 56: 560 (1991); *OLIGODEOXYNUCLEOTIDES AS ANTISENSE INHIBITORS OF GENE EXPRESSION*, CRC Press, Boca Raton, FL (1988), for a description of these molecules). Preferred potential antagonists include compounds related to and variants of a polypeptide of the invention.

Each of the DNA sequences provided herein may be used in the discovery and development of antibacterial compounds. The encoded protein, upon expression, can be used as a target for the screening of antibacterial drugs. Additionally, the DNA sequences encoding the amino terminal regions of the encoded protein or Shine-Delgarno or other translation facilitating sequences of the respective mRNA can be used to construct antisense sequences to control the expression of the coding sequence of interest.

The invention also provides the use of the polypeptide, polynucleotide or inhibitor of the invention to interfere with the initial physical interaction between a pathogen and mammalian host responsible for sequelae of infection. In particular the molecules of the invention may be used: in the prevention of adhesion of bacteria, in particular gram positive bacteria, to mammalian extracellular matrix proteins on in-dwelling devices or to extracellular matrix proteins in wounds; to block protein-mediated mammalian cell invasion by, for example, initiating phosphorylation of mammalian tyrosine kinases (Rosenshine *et*



*al.*, *Infect. Immun.* 60:2211 (1992); to block bacterial adhesion between mammalian extracellular matrix proteins and bacterial proteins that mediate tissue damage and; to block the normal progression of pathogenesis in infections initiated other than by the implantation of in-dwelling devices or by other surgical techniques.

The antagonists and agonists of the invention may be employed, for instance, to inhibit and treat disease.

*Helicobacter pylori* (herein *H. pylori*) bacteria infect the stomachs of over one-third of the world's population causing stomach cancer, ulcers, and gastritis (International Agency for Research on Cancer (1994) Schistosomes, Liver Flukes and *Helicobacter Pylori* (International Agency for Research on Cancer, Lyon, France; <http://www.uicc.ch/ecp/ecp2904.htm>). Moreover, the international Agency for Research on Cancer recently recognized a cause-and-effect relationship between *H. pylori* and gastric adenocarcinoma, classifying the bacterium as a Group I (definite) carcinogen. Preferred antimicrobial compounds of the invention found using screens provided by the invention, particularly broad-spectrum antibiotics, should be useful in the treatment of *H. pylori* infection. Such treatment should decrease the advent of *H. pylori*-induced cancers, such as gastrointestinal carcinoma. Such treatment should also cure gastric ulcers and gastritis.

#### **Vaccines**

Another aspect of the invention relates to a method for inducing an immunological response in an individual, particularly a mammal which comprises inoculating the individual with a polypeptide of the invention, or a fragment or variant thereof, adequate to produce antibody and/ or T cell immune response to protect said individual from infection, particularly bacterial infection and most particularly *Streptococcus pneumoniae* infection. Also provided are methods whereby such immunological response slows bacterial replication. Yet another aspect of the invention relates to a method of inducing immunological response in an individual which comprises delivering to such individual a nucleic acid vector to direct expression of a polynucleotide or polypeptide of the invention, or a fragment or a variant thereof, for expressing such polynucleotide or polypeptide, or a fragment or a variant thereof *in vivo* in order to induce an immunological response, such as, to produce antibody and/ or T cell immune response, including, for example, cytokine-producing T cells or cytotoxic T cells, to protect said individual from disease, whether that disease is already established within the individual or not. One way of administering the gene is by accelerating it into the desired cells as a coating on particles or otherwise. Such

nucleic acid vector may comprise DNA, RNA, a modified nucleic acid, or a DNA/RNA hybrid.

A further aspect of the invention relates to an immunological composition which, when introduced into an individual capable or having induced within it an immunological response, induces an immunological response in such individual to a polynucleotide of the invention or protein coded therefrom, wherein the composition comprises a recombinant polynucleotide or protein coded therefrom comprising DNA which codes for and expresses an antigen of said polynucleotide or protein coded therefrom. The immunological response may be used therapeutically or prophylactically and may take the form of antibody immunity or cellular immunity such as that arising from CTL or CD4+ T cells.

A polypeptide of the invention or a fragment thereof may be fused with co-protein which may not by itself produce antibodies, but is capable of stabilizing the first protein and producing a fused protein which will have immunogenic and protective properties. Thus fused recombinant protein, preferably further comprises an antigenic co-protein, such as lipoprotein D from *Hemophilus influenzae*, Glutathione-S-transferase (GST) or beta-galactosidase, relatively large co-proteins which solubilize the protein and facilitate production and purification thereof. Moreover, the co-protein may act as an adjuvant in the sense of providing a generalized stimulation of the immune system. The co-protein may be attached to either the amino or carboxy terminus of the first protein.

Provided by this invention are compositions, particularly vaccine compositions, and methods comprising the polypeptides or polynucleotides of the invention and immunostimulatory DNA sequences, such as those described in Sato, Y. *et al.* Science 273: 352 (1996).

Also, provided by this invention are methods using the described polynucleotide or particular fragments thereof which have been shown to encode non-variable regions of bacterial cell surface proteins in DNA constructs used in such genetic immunization experiments in animal models of infection with *Streptococcus pneumoniae* will be particularly useful for identifying protein epitopes able to provoke a prophylactic or therapeutic immune response. It is believed that this approach will allow for the subsequent preparation of monoclonal antibodies of particular value from the requisite organ of the animal successfully resisting or clearing infection for the development of prophylactic agents or therapeutic treatments of bacterial infection, particularly *Streptococcus pneumoniae* infection, in mammals, particularly humans.

The polypeptide may be used as an antigen for vaccination of a host to produce specific antibodies which protect against invasion of bacteria, for example by blocking adherence of bacteria to damaged tissue. Examples of tissue damage include wounds in skin or connective tissue caused, e.g., by mechanical, chemical or thermal damage or by implantation of indwelling devices, or wounds in the mucous membranes, such as the mouth, mammary glands, urethra or vagina.

The invention also includes a vaccine formulation which comprises an immunogenic recombinant protein of the invention together with a suitable carrier. Since the protein may be broken down in the stomach, it is preferably administered parenterally, including, for example, administration that is subcutaneous, intramuscular, intravenous, or intradermal. Formulations suitable for parenteral administration include aqueous and non-aqueous sterile injection solutions which may contain anti-oxidants, buffers, bacteriostats and solutes which render the formulation isotonic with the bodily fluid, preferably the blood, of the individual; and aqueous and non-aqueous sterile suspensions which may include suspending agents or thickening agents. The formulations may be presented in unit-dose or multi-dose containers, for example, sealed ampules and vials and may be stored in a freeze-dried condition requiring only the addition of the sterile liquid carrier immediately prior to use. The vaccine formulation may also include adjuvant systems for enhancing the immunogenicity of the formulation, such as oil-in water systems and other systems known in the art. The dosage will depend on the specific activity of the vaccine and can be readily determined by routine experimentation.

While the invention has been described with reference to certain protein, such as, for example, those set forth in Table 1, it is to be understood that this covers fragments of the naturally occurring protein and similar proteins with additions, deletions or substitutions which do not substantially affect the immunogenic properties of the recombinant protein.

#### **Compositions, kits and administration**

The invention also relates to compositions comprising the polynucleotide or the polypeptides discussed above or their agonists or antagonists. The polypeptides of the invention may be employed in combination with a non-sterile or sterile carrier or carriers for use with cells, tissues or organisms, such as a pharmaceutical carrier suitable for administration to a subject. Such compositions comprise, for instance, a media additive or a therapeutically effective amount of a polypeptide of the invention and a pharmaceutically acceptable carrier or excipient. Such carriers may include, but are not limited to, saline, buffered saline, dextrose, water, glycerol, ethanol and combinations thereof. The formulation should suit the mode of administration. The

invention further relates to diagnostic and pharmaceutical packs and kits comprising one or more containers filled with one or more of the ingredients of the aforementioned compositions of the invention.

Polypeptides and other compounds of the invention may be employed alone or in conjunction with other compounds, such as therapeutic compounds.

The pharmaceutical compositions may be administered in any effective, convenient manner including, for instance, administration by topical, oral, anal, vaginal, intravenous, intraperitoneal, intramuscular, subcutaneous, intranasal or intradermal routes among others.

In therapy or as a prophylactic, the active agent may be administered to an individual as an injectable composition, for example as a sterile aqueous dispersion, preferably isotonic.

Alternatively the composition may be formulated for topical application for example in the form of ointments, creams, lotions, eye ointments, eye drops, ear drops, mouthwash, impregnated dressings and sutures and aerosols, and may contain appropriate conventional additives, including, for example, preservatives, solvents to assist drug penetration, and emollients in ointments and creams. Such topical formulations may also contain compatible conventional carriers, for example cream or ointment bases, and ethanol or oleyl alcohol for lotions. Such carriers may constitute from about 1% to about 98% by weight of the formulation; more usually they will constitute up to about 80% by weight of the formulation.

For administration to mammals, and particularly humans, it is expected that the daily dosage level of the active agent will be from 0.01 mg/kg to 10 mg/kg, typically around 1 mg/kg. The physician in any event will determine the actual dosage which will be most suitable for an individual and will vary with the age, weight and response of the particular individual. The above dosages are exemplary of the average case. There can, of course, be individual instances where higher or lower dosage ranges are merited, and such are within the scope of this invention.

In-dwelling devices include surgical implants, prosthetic devices and catheters, i.e., devices that are introduced to the body of an individual and remain in position for an extended time. Such devices include, for example, artificial joints, heart valves, pacemakers, vascular grafts, vascular catheters, cerebrospinal fluid shunts, urinary catheters, continuous ambulatory peritoneal dialysis (CAPD) catheters.

The composition of the invention may be administered by injection to achieve a systemic effect against relevant bacteria shortly before insertion of an in-dwelling device.

Treatment may be continued after surgery during the in-body time of the device. In addition, the composition could also be used to broaden perioperative cover for any surgical technique to prevent bacterial wound infections, especially *Streptococcus pneumoniae* wound infections.

Many orthopedic surgeons consider that humans with prosthetic joints should be considered for antibiotic prophylaxis before dental treatment that could produce a bacteremia. Late deep infection is a serious complication sometimes leading to loss of the prosthetic joint and is accompanied by significant morbidity and mortality. It may therefore be possible to extend the use of the active agent as a replacement for prophylactic antibiotics in this situation.

In addition to the therapy described above, the compositions of this invention may be used generally as a wound treatment agent to prevent adhesion of bacteria to matrix proteins exposed in wound tissue and for prophylactic use in dental treatment as an alternative to, or in conjunction with, antibiotic prophylaxis.

Alternatively, the composition of the invention may be used to bathe an indwelling device immediately before insertion. The active agent will preferably be present at a concentration of 1µg/ml to 10mg/ml for bathing of wounds or indwelling devices.

A vaccine composition is conveniently in injectable form. Conventional adjuvants may be employed to enhance the immune response. A suitable unit dose for vaccination is 0.5-5 microgram/kg of antigen, and such dose is preferably administered 1-3 times and with an interval of 1-3 weeks. With the indicated dose range, no adverse toxicological effects will be observed with the compounds of the invention which would preclude their administration to suitable individuals.

Each reference disclosed herein is incorporated by reference herein in its entirety. Any patent application to which this application claims priority is also incorporated by reference herein in its entirety.

## TABLES

Certain pertinent data for preferred polypeptide and polynucleotide embodiments of the invention are summarized in Tables 1 and 2.

Provided in Table 1 are sequence search results providing characterization information regarding certain preferred polynucleotides (denoted as "Assembly") and polypeptides of the invention encoded thereby. For each polynucleotide in Table 1, there is listed the closest homologue of each polypeptide encoded by each ORF in such polynucleotide. This determination of homology is based on a comparison of the sequences

of in Table 1 with sequences available in the public domain (see heading entitled "Description" for the homologue name). Where no significant homologue was detected the term "unknown" appears after the heading "Description". Preferred polypeptides encoded by the ORFs of the invention, particularly full length proteins either obtained using such ORFs or encoded entirely by such ORFs, are ones that have a biological function of the homologue listed, among other functions. The analysis used to determine each homologue listed in Table 1 was either BlastP and/or BlastX and/or MPSearch, each of which is well known. Also provided in Table 1 is the amino acid sequence encoded by each ORF. An "Assembly ID" number provides a convenient way to correlate the polynucleotide sequence with the ORF or ORFs it comprises and the polypeptides encoded by these ORFs, as well as to correlate such sequences with other pertinent information provided in Tables 1 and 2. Following the heading "ORF Predictions" the nucleotides at the beginning and end of the ORF sequence are set forth ("Start" and "End" respectively). The direction of translation on the polynucleotide depicted is denoted by an "F" for forward or an "R" for reverse (reverse being translated on the opposite strand from the one depicted). The length of each amino acid sequence is also indicated in a column entitled "Length." Below these data is shown the amino acid sequence encoded by the ORF. If a given polynucleotide comprises one ORF, then in the column entitled "ORF #" there is the numeral one. If it encodes two, there are the numerals one and two in the column, and so on.

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**TABLE 1**

Assembly ID: 3047950

Assembly Length: 587bp

```
[SEQ ID NO:      ] 3047950 Strep Assembly -- Assembly
id#3047950
CTCAGTTCTTGCCATCCTTCTTCCTCGCTTTTTTGATGAAACTGCCCTTCATATCTACAC
GCTTGTCCAGATAGCGATAAACGCGCTGATATCCATCTCCCATGAAATAGGTTGGGGCAA
ACAGTTGATTTTTTAAATGTCCCTTTTCATCCAGGAATTCTGGGGCAACAAGTCGCTCAA
GAATCTTGCCAAAGATGTGGCAAATACCGTCTTCCTCAACAATCCTATCTACCCGACAAT
CTAAAACAAGTGGACAGGCGTCTAAAATAGAAATCTGAGTTCGTTTCAGAAATTTTCATAAT
GCACTCCCAAACGTTCCAATTTCTCCTGATGACTGATAAAACCAGCCTGCTCCATCGCAA
GCATAGAAGTTTCATCAGAAATATTACAGTAAATTTTTGATACTGTTTGATCTGCTCTG
CGGCATTCTCTCTCGCAACGACTCCAATCACAACCAATCTCCTAGACTATAAGAAGAAC
TACAGGTCGTGATGTTATAGCCAAATTTCTAATCTTGATATCCTAAAATAAAAACAGGAA
AACCATAATATAGTTTACTTGTGTTAAAAGATTGCTTCATAACAACC
```

## ORF Predictions:

ORF #	Start	End	Direction	Length
6	2	451	R	150 aa

[SEQ ID NO: ] 3047950-6 ORF translation from 2-451,  
 direction R  
 VIGVVARENAAEQIKQYQKFTVNISDETSMLAMEQAGFISHQEKLERLGVHYEISERTQI  
 SILDACPLVLDCRVDRIVEEDGICHIFAKILERLVAPEFLDEKGHFKNQLFAPTYFMGDG  
 YQRVYRYLDKRVDMKGSFIKKARKKDGKN\*

## Blastp and/or MPSearch Result:

Description:  
 unknown

Assembly ID: 3049152  
 Assembly Length: 468bp

[SEQ ID NO: ] 3049152 Strep Assembly -- Assembly  
 id#3049152  
 CTCCTAGTTTGCTCTTTGATTTTCATTGACTATAAATGGTTTTAATTCTTTTTTTTCAAA  
 TCTGGCACTACTTCTGCCTCAAACCAAGGATTTTTGGCCATCCAGATTTGATTTTCGTGGT  
 GATGGGTGAAGTAGCGGAAAATAGGCTGGCAGATAGTCTTTATAGTGTTCACCTCTCC  
 GTTACCTTCCCACTGATTTTCTCCTGTAAATAGTAGGCTTGGGCATATTGCCCAATCAAG  
 AGGGTTAACTGAATATCAGGCAATTCCTGTAAGAGCTGCGGATGCCATTTTTCTGCAAAA  
 CCTGTACGAGGCGGAAGATCACCCGACTTGCCATGTCCTGGAAAGTTAGAAATCCATAGG  
 CAAAACAGCAAAATAACCTGAATTGTAAAAGGTATCTTCATCCACACCTAGCCAGTCCCC  
 GCAAGCGGTCACCACTTTTATCTTTCCAGTAAGCCTGCTTCCTTGATT

## ORF Predictions:

ORF #	Start	End	Direction	Length
-------	-------	-----	-----------	--------

-----  
 6                    24                    407                    R                    128 aa

[SEQ ID NO:        ]    3049152-6 ORF translation from 24-407,  
 direction R  
 VWMKIPFTTIQVILLFCLWISNFPGHGKSGDLPPRTGFAEKWHPQLLQELPDIQLTLLIGQ  
 YAQAYYLQEKISGKVTERVKHYKDYLPAFYFPLVHPSPRNQIWMAKNPWFEAEVVPDLKKR  
 IKTIYSQ\*

Blastp and/or MPSearch Result:

Description:  
 unknown

Assembly ID:    3174820  
 Assembly Length: 1086bp

[SEQ ID NO:        ]    3174820 Strep Assembly -- Assembly  
 id#3174820  
 CTACCTTGCTAGATGTGATAGACCGTGGAATGTCTCTATCATTTTCAGAAGGAGATGCAG  
 TTGGTTTGTAGGCTAGTAAAAGAAGATGGTTTGTCAAGCTTTGAGAAAGACTGCCTAAATC  
 TAGCTTTTTCAGGTAAAAAGAAGAACTCTTTCCAATTTGTTTGCAGGATTACAAGGTAT  
 CTGATAGTCTTTATCGTAGAGCCAAAGTTTCTGATGAAAAACGGATTCAAGCAAGAGGGC  
 TTCAACTCAAATCTTCTTTTGAAGAGGTATTGAACCAGATGCAAGAAGGAGTGAGAAAAC  
 GAGTTTCCTTCTGGGGGCTCCCAGATTACTATCGTCCTTTAACTGGTTTGGAAAAGGCTT  
 TGCAAGTGGGTATGGGTGTCTTGACTATCTTGCCCCCTATTTATCGGATTTGGTTTGTTC  
 TGTACAGTTTAGACGTTTCATGGCTATCTTTACCTCCCTTTGCCAATACTTGGTTTCTAG  
 GGTTAGTTTGTCTGTTTTCTATTATTGGAAGCTTCGACTAGATAATCGTGATGGTGTTCT  
 TAAATGAAGCGGGAGCTGAGGTCTACTATCTCTGGACCAGTTTGAAGATATGTTACGTG  
 AGATTGCACGACTGGATAAGGCTGAATTGCGAAAGTATTGTTGTTTGGAAATCGTCTCTTG  
 GTCTATGCAACCTTATTTGGCTATGCGGACAAGGTTAGTCATTTGATGAAGGTTTCATCAG  
 ATTCAGTTGAAAATCCAGATATCAATCTCTATGTAGCTTATGGCTGGCACAGTATGTTT  
 TATCATTCGAAGCGCGCAAATGAGCCATTATGCTAGTGTGCGCAAATACAGCAAGTACCTAC  
 TCCGTATCTTCTGGAAGTGGAAGTCTGGTGGTGGCTTCTCTGGAGGCGGAGGTGGCGGCA  
 GTATCGGTGCCTTTTAAAGAGAGCTACCATACTGAAAAAGTATGATATATGGAAGATA  
 GAAAAAGACACCTATANGAAAATCATAGTTTTATCTAACTATTTCTTATTTCCATTGAT  
 GATTTTGGCGAAGAATTTTAGAACCCGGCAAAAAGCCCTTGAAAAATTCCATTTTCCAA



AGGTAA

## ORF Predictions:

ORF #	Start	End	Direction	Length
7	598	1041	F	148 aa

[SEQ ID NO: ] 3174820-7 ORF translation from 598-1041,  
direction F  
VRLHDWIRLNCESIVVWNRLLVYATLFGYADKVSFLMKVHQIQVENPDINLYVAYGWHSM  
FYHSSAQMSHYASVANTASTYSVSSGSGSLVVASLEAEVAASVVPFKESYHTLKKYDIWK  
IEKDTYXKIIIVLSKLFLISIDDFGEEF\*

## Blastp and/or MPSearch Result:

Description:  
unknown

Assembly ID: 3175500  
Assembly Length: 1284bp

[SEQ ID NO: ] 3175500 Strep Assembly -- Assembly  
id#3175500  
CTCATTTGCAAAATCAGGAAAAACGGATGGTAACGGCAGTCCGAAATGTTCTATCTAAGA  
AACAGAGGCTTTGAAAAAATGCAGTCAGTCTGTTATCTTTAGACAACCTGAGCGCTTGT  
ATGACGGTTATTTGCAACGCTTGGACCAACTGCAACTGCGTTTGAAACAAAGTTTGCGAA  
CTCGGATTTCTGATAACAAACAATTAGTTCAAGCAAGAACTCATCAATTAGTACAATTAT  
CACCTGTTACCAAAATCCAACGCTATCAAGACCGTTTAGGACAGTTGGACAAGCTTCTTA  
GGTAGCCAAATGGCGTTAGTTTATGACGCCAAGGTTGCTGAGGCCAAGCGACTTTCGGAA  
GCTTTGCTCATGTTGGATACTAGCCGAATCGTGGCGCGTGGTTATGCTATTGTCAAAAAA  
GAAGAATCCGTTGTAGATTCGGTTGAGAGTTTGAAGAAAAAAGACCAAGTAACGCTTTTG  
ATGCGAGATGGTCAAGTAGAATTAGAGGTTAAAGATGTCAAAACAAAAGAAATTTGAGGA  
AAATCTAGCAGAACTGGAAACCATTTGTCCAAAGTTTGGAAAATGGTGAAATTGCTCTGGA  
AGATGCGATTACTGCCTTTCAAAAGGGCATGGTCTTGTCAAAAGAGCTCCAAGCTACGCT  
GGACAAGGCTGAAAAGACCTTGGTCAAGGTCATGCAAGAAGACGGAACAGAAAGTGATTT

TGAATGAAAAAGCAAGAAAAATTAGCTCTTGTGCGAGTCGGCTTTGGAAGATTTTATGGAG  
 ACCAGCAGTTTGCCTCTAGTTTACGGGAGTCTGTTCTCTATTCTATTCATGCTGGTGGCA  
 AGCGTATTCGGCCTTTTCTCTTGTTAGAAGTTCTGGAAGCCTTGCAGGTTACCATCAAAC  
 CTGCTCNCGCGCAGGTAGCTACTGCCTTGGAGATGATTCATACAGGGAGCTTGATTCACG  
 ATGACCTTCCTGCTATGGATGATGACGAGGATCGAGAGAGGGCGGAAAAACCAATCACAA  
 GAAATCCGGTGAAGCTATGGCCATCCTAGCTGGAGATGCCTCATGCTTAGACCCATATGC  
 CTTGATTGCGCAGGCAGATCCGCCAAGTCAGATCAAGGTGGGCTCGATTGCCAACTCATC  
 CCTTGCTTCAGGTAGCCTGGGTATGGTGGCAGGGCAAGTCTTGATATGGAGGGCGAACA  
 CCAGCACTGGTCTCTGGAAGAACTTCAGACTATGCATGCCAACAAGACTGGGAAGTTACT  
 AGCCTATCCCTTCCAACGCGGCAG

## ORF Predictions:

ORF #	Start	End	Direction	Length
8	714	1049	F	112 aa

[SEQ ID NO: ] 3175500-8 ORF translation from 714-1049,  
 direction F  
 VILNEKARKISSCRVGFGRFYGDQQFASSLRESVLYSIHAGGKRIRPFLLLLEVLEALQVT  
 IKPAXAQVATALEMIHTGSLIHDDLPMDDDEDREAEKPITRNPVKLWPS\*

## Blastp and/or MPSearch Result:

## Description:

GERANYLTRANSTRANSFERASE (EC 2.5.1.10) (FARNESYL-DIPHOSPHATE  
 SYNTHASE) (FPP SYNT HASE). - BACILLUS STEAROTHERMOPHILUS.

Assembly ID: 3175674  
 Assembly Length: 816bp

[SEQ ID NO: ] 3175674 Strep Assembly -- Assembly  
 id#3175674  
 CTGTTGGAAACTAGGTGCTTTTAAATTGCCAGTAGAAGTGGTTCAGTATGGTGCAGAGC  
 AGTCTTTCGTCATTTTGAACGAGCTGGTACCAAACAAGTTCCGTGAAAAAGACGCCAAC  
 GTTTTGTGACGGATATGCAGAATTTTATCATTGACCTCGCCTTGGATGTCATTGAAAATC

CAATTGCTTTTGGACAAGAATTGGACCATGTCGTTGGTGTGTGGAGCATGGTTTATTCA  
 ACCAAATGGTGGATAAGGTAATCGTTGCTGGACGAGATGGAGTTCAGATTTCAACTTCAA  
 AAAAAGGAAAATAGAAGGGGGCATAAGATGTCTAAATTTAATCGTATTCATTTGGTGGTA  
 CTGGATTCTGTAGGAATCGGTGCAGCACCAGATGCTAATAACTTTGTCAATGCAGGGGTT  
 CCAGATGGAGCTTCTGACACACTGGGACACATTTCAAAAACAGTTGGTTTGAATGTCCCA  
 AACATGGCTAAAATAGGTCTTGGAATATTCCTCGTGAAACTCCTCTTAAGACTGTAGCA  
 GCTGAAAGCAATCCAACCTGGATATGCAACAAAATTAGAGGAAGTATCTCTTGGTAAGGAT  
 ACTATGACTGGACACTGGGAAATCATGGGACTCAACATTACTGAGCCTTTTCGATACTTTC  
 TGGAACGGATTCCCAGAAGAAATCCTGACAAAAATCGAAGAATTCTCAGGACGCAAGGTT  
 ATTCGTGAAGCCAACAAACCTTATTCAGGAACGGCTGTTATCGATGATTTTGGACCACGT  
 CAGATGGAAACTGGAGAGTTGATATCTATACTTCAG

## ORF Predictions:

ORF #	Start	End	Direction	Length
6	126	314	F	63 aa

[SEQ ID NO: ] 3175674-6 ORF translation from 126-314,  
 direction F  
 VTDMQNFIIDLALDVIENPIAFGQELDHVVGVEHGLFNQMVDKVIVAGRDGVQISTSKK  
 GK\*

## Blastp and/or MPSearch Result:

Description:  
 unknown

Assembly ID: 3176442  
 Assembly Length: 617bp

[SEQ ID NO: ] 3176442 Strep Assembly -- Assembly  
 id#3176442  
 CTAGTACAGCTTATGCGGCCCGTTTTATTTCCGAACATCCAGATCAGCCCTTTGCAGCAA  
 TTGCACCCAGAATTTCTGCTGAAGAATATGGATTGGAAGTATTGCCGAGGATATTCAGG  
 AAATGGAAGCCAATTTACACGTTTCTGGCTTCTAGGAGCTGAAAAGCCTAGTATTCCT

TGCAAGCACAAACTGAAAAGATGAGTTTGGCCTTGACATTACCTGACAACCTTCCAGGTG  
 CACTTTTATAAGGCCCTGTGACCTTTGCTTGGCGAAGGGAATTGACTTGACAAAAATTGA  
 AAGTCGTCCACTCAAGACAGCACTGGGTGAATACTTTTTCATTATCGATGTGGATTATAC  
 CGATAAGGACTTGGTCCACTTTGCCCCAAAAAGAATTAGAAGCGATTGGAATCCAGTATAA  
 AATTCTGGGTGCCTATCCTATTTATCCAATATCAGACCATGGAAAGGAGAGAAGATGAGT  
 AAAGAAAATCCCTTAAGTCATCATGAGCAGTTGCGTTATGATTATTTGCTAAAAAATATT  
 CACTATCTCAATGAGAGAGAAAAAATGAGTTTGTCTATTTGCAAGAAAAGCTAACTCTT  
 GCTAGGGGAAATAGTAG

## ORF Predictions:

ORF #	Start	End	Direction	Length
6	350	478	F	43 aa

[SEQ ID NO: ] 3176442-6 ORF translation from 350-478,  
 direction F  
 VDYTDKDLVHFAQKELEAIGIQYKILGAYPIYPISDHGKERR\*

## Blastp and/or MPSearch Result:

Description:  
 unknown

Assembly ID: 3176630  
 Assembly Length: 457bp

[SEQ ID NO: ] 3176630 Strep Assembly -- Assembly  
 id#3176630  
 CCAGTCATCAAATTGACCAAATTGAGAGTCAAATTACTTTGATTGAAAAAATATTGCGG  
 CAATTCGCAATGCTTTGGCAGACTTAGAGAAGCAAGAATCTAAAAATAGTGGTCGTGTTT  
 TTCATGCTTCGGATTTATTTGAGGAACCTTCAGCATAAAGTTGCTGAAAATTCAGAACGT  
 ATGGTCAAGCCTTGGATGAAATTGAAAAACAATGAGAAAATATCCAATCTGAATTTTCAC  
 AATTTGTAACCTTGAATTCATCGGGTGACCCTGTGGAAGCCGCAGTGATTTTGGATAATA  
 CAGAAAATCACATTTTGGCCTTAAGTCATATTGTGGATCGTGTTCCAGCCTTGGTTACGA  
 CCTTTCTACAGAATTGCCAGATCAATTACAGGGATTTGGAACCGGTTATCGTAAACTAAT

TGATGCTAATTATCATTTTGTGAAACGGATATGGAA

ORF Predictions:

ORF #	Start	End	Direction	Length
6	273	419	F	49 aa

[SEQ ID NO: ] 3176630-6 ORF translation from 273-419,  
direction F  
VEAAVILDNTENHILALSHIVDRVPALVTTFLQNCQINYRDLEPVIVN\*

Blastp and/or MPSearch Result:

Description:  
unknown

Assembly ID: 3176662  
Assembly Length: 381bp

[SEQ ID NO: ] 3176662 Strep Assembly -- Assembly  
id#3176662  
CTTATTTAGTACGCATTTCCCCTTGTGGGAAGTAAGTTCCTTCTGGCATGTCGTTGATGA  
TGACATGGACAGCAGATTGAGGGGCTCCAGTGTTGCGGACAACCTGCTTCCGTTACTTCCT  
TAGCAAGAGCTTTCTTTTGCTCGAGCGTGCGTCCTTCAAATAAATCGATGCGTACAAATG  
GCATAATAGCTTCCTCCACTAGTTTTGATTTCTTCCATTTTACCACATTTTGCCGTTTAA  
AGCTTAAGAAAATTATGATATACTAGAATGTAGCAAAAATTTAGAAATGGACGTGAAGCA  
AGAAACATGGCACAGTTGTACTATCGTTATGGGACCATGAACTCTGGTAAAACGATTGAG  
ATTCTCAAAGTGGCCTATAAC

ORF Predictions:

ORF #	Start	End	Direction	Length
6	2	226	R	75 aa

[SEQ ID NO:     ]     3176662-6 ORF translation from 2-226,  
direction R  
VVKWKKSCLVEEAIMPFVRLDLFEGRTLQKKALAKEVTEAVVRNTGAPQSAVHVIINDM  
PEGTYFPQGEMRTK\*

Blastp and/or MPSearch Result:

Description:

4-OXALOCROTONATE TAUTOMERASE (EC 5.3.2.-). - PSEUDOMONAS  
PUTIDA.

Assembly ID:   3857692  
Assembly Length: 743bp

[SEQ ID NO:     ]     3857692 Strep Assembly -- Assembly  
id#3857692  
CTGGCAAATACAAGGTGACGATCATTGGTAAATCAGCCCACGGTGCTATGCCTGCTTCAG  
GTGTCAATGGTGCGACTTACCTAGCCCTCTTCCTTAGCCAGTTTGACTTTGCTGGTCCAG  
CCAAAGAATACCTTGACATCACTGGTAAAATTCTCTTGAACGACCATGAGGGTGAAAGTC  
TCAAGATTGCTCATGTGGATGAAAAGATGGGTGCCCTTTCTATGAATGCAGGCGTCTTCC  
GCTTCGATGAAACAAGTGCTGATAATACCATTGCCCTCAACATCCGCTATCCAAAAGGAA  
CAAGTCCAGAACAAATCAGTCAATCCTTGAAAACCTTGCCAGTTGTTTCTGTTAGCCTGTC  
TGAACACGGTCACACGCCTCACTATGTGCCAATGGAAGATCCACTTGTGCAAACCTTGTT  
GAATGTCTATGAAAAACAAACAGGCCTTAAAGGTCATGAACAAGTCATCGGTGGTGGAAC  
CTTTGGTCGCTTGTTAGAGCGCGGAGTTGCCTATGGTGCTATGTTCCCAGACTCAATTGA  
TACCATGCACCAAGCCAATGAATTTATTGCCTTGATGATCTCTTCCGAGCAGCAGCAAT  
TTATGCCGAAGCTATTTACGAATTGATCAAATAAAACGATAGAAGTCTGAGATCTTATGC  
TTGGACTTCTTTTGGAGGGAAAGTAGATGTCTCAAATCGAAAGAATCAAACAGGCTATC  
ATGGCGGATTACAGAATGCCAG

ORF Predictions:

ORF #	Start	End	Direction	Length
6	386	634	F	83 aa

[SEQ ID NO: ] 3857692-6 ORF translation from 386-634,  
direction F  
VPMEDPLVQTLNVEKQTGLKGHEQVIGGGTFGRLLERGVAYGAMFPDSIDTMHQANEF  
IALDDLFRAAAIYAEAIYELIK\*

Blastp and/or MPSearch Result:

Description:

XAA-HIS DIPEPTIDASE (EC 3.4.13.3) (X-HIS DIPEPTIDASE)  
(AMINOACYL- HISTIDINE DIPEPTIDASE) (CARNOSINASE). -  
LACTOBACILLUS DELBRUECKII (SUBSP. LACTIS). (BLAST)

Assembly ID: 3857944

Assembly Length: 1783bp

[SEQ ID NO: ] 3857944 Strep Assembly -- Assembly  
id#3857944

CCACGGTGGAGGGTTGCAAAGTAAGCGACGAATTGCGTTGGTACGACCATTGAAATTGGT  
GAGAGGTATGGATGTACGGTCGTAAGGACGATATCGTCGGTATCTTTGGCTACATTCTCT  
TCTACGATAGTGAGGACTTTGGCACACGGGCTGCGACCTCTTGATATTTCCACGAGTA  
TGTTTGGCAAGAAGTGGATCTGACAAGAGAGCCAAAACAGGCGTTCCTTCTTCAATCAAG  
GCAATGGTTCCGTGCTTGAGTTCTCCTGCTGCAAACCTTCACACTGGATATAAGAAATC  
TCTTTGAGTTTGAGACTTGCTTCCATGGCTACGTAGTAATCTTGACCACGTCCGATGTAA  
AAGGCGTTACGAGTTGTTTCAAGAAGTCCACGAACCTTGACTTCAATGGTTTCTTTCTCT  
GAAAGAGTTGATTCCAATAGACTGAGCTACGATTGACAAATTCATGAACCAGGTCAAAGGC  
TTGCGCTTTAGCATTACCATTTGCTTCTCCGACTGCTTTTGCAAGGAAGGCAAGGGCTGC  
GATTTGCGCTGTATAGGCTTTAGTTGATGCCACGGCAATTTACAGGACCTGCGTGAAGGAG  
CATGGTATAGTTGGCTTCACGTGAGAGGGTTGAACCTGGAACATTTGTCACTGTTAAGCT  
TGGAATTTCCATTTTATTAGCCTTGACCAAACTTGACGACTATCCGCTGTTTCACCAGA  
TTGGCTGATAAAGATGAAGAGTGGTTTCTTGCTGAGAAGTGGCATAACCGTAGCCCCACTC  
AGATGAAATTTCAAGTTCAACTGGTGTATCTGTCAATTTCTTCCAACATTTTCTTAGAAGC  
AAATCCTGCATGGTAAGATGTTCCAGCTGCAAGGATGTAGATGCGGTCTGCGTCTTGAAC  
AGCCTTAATGATAGCAGGATCAACCACTACTTGACCAGCATCATCCGTGTAGGCTTGAAT  
GAGTTTACGCATAACAGTTGGTTGCTCATCAATTTCTTAAAGCATGTAGTAAGGATAAGT  
TCCCTTACCGATATCTGACAAGTCAAGTTCCGCAGTATAGCTAGCACGTTTACGACTGTT  
ACCATCATAGTCTTGGAACCTTCCACGCTATCAGCCTTGACGATTACCAACTCTTGGTCAT

GGATTTCCATGTATTGGTTAGTTTCACGAATCATAGCCATGGCGTCTGAGCAGACCATGT  
TATAGCCTTCTCCAAGACCAATCAAAAGTGGTGATTTATTTATAGCTACGTAGATGACTT  
CAGGATCTTGTGAGTCAACCAAGGCAAAGGCATAAGAACCACGGATGATGTGAAGGGCTT  
TTTTGAAGGCTTCAAGAACTGAGAGCCCTTCTTCTTCCGGCAAATTTTCCAATCAAATGA  
ACGGCTATTTTCAGTATCTGTCTGCCCCCTTGAAGTGGTGACCTGCAAGGTATTCTTCCTTG  
ATTTCAAGATAGTTCTCAATCACCCCATTATGCACCAAGACAAAACGTTCTGTCTCAGAG  
CGGTGTGGGTGAGCATTTGTCTCAGTTGGTTTTCCGTGAGTAGCCCAACGAGTATGTCCG  
ATACCAGTTGTTCCCTCAACACCGGCTGTCTTGGCAGACAATTCGATGCAATACGACCAA  
CCGCCTTCACCAAATGGTTATCAGCACCATTTAGGACAAAAATTCCCGCAGAATCATAGC  
CACGGTATTCAAGCTTTTCAAGCCCTTGAATCAAAATATCAGTTGCATTTGTGTTTCCAA  
CAACACCAACAATTCCACACATAGTATATACGACACAGGCAAG

## ORF Predictions:

ORF #	Start	End	Direction	Length
7	1332	1475	R	48 aa

[SEQ ID NO: ] 3857944-7 ORF translation from 1332-1475,  
direction R  
VHNGVIENYLEIKEEYLAGHHFKGQTDTEIAVHLIGKFAGRRRALSS\*

## Blastp and/or MPSearch Result:

## Description:

PROBABLE GLUCOSAMINE--FRUCTOSE-6-PHOSPHATE AMINOTRANSFERASE  
(ISOMERIZING) (EC 2.6.1.16) BSU21932 NCBI gi: 726479 -  
Bacillus subtilis.

Assembly ID: 3858118

Assembly Length: 1729bp

[SEQ ID NO: ] 3858118 Strep Assembly -- Assembly  
id#3858118  
CTCAGCTACTTCGCCTTTCTTTTTATTCTACTGGTTTTCTTGATTTCCAGTAGTTGTAG  
AAGATTCTGTTGTTTTATTTTCTGAAGTTGATTCAGCAGGTTTAGAATCTCTTGATTGC



TTGGTTTGTTCGTCGCTAGCAGTTTCAATGTTAGATTCTGCAGTTGCGTTTGGTTGGT  
TCTCAGCACTGGTGTATCACCATTGCTTCAGCATTTCTTGCTGGACTTGTTCCTCAC  
TTGCGCTAGCTTTTGACTGGATTTGATGATTCAAACTAGAATAGCTTTTGTGCGATTCAA  
GTAAAGCTGTTTTGTCTTTACTATTAGCAGAAAGTTGATCTAATAATGCATCCACCTTAT  
CAAAAGTCCGCATCAGATCCATTATTACTTTCTAAATAAAAGTGAAGCGACATGAGAATA  
TCGTAGAGTTTTTGATAGAGTACAAGTGTCTGAGGATCTTGCTCAGCATTTTCCTTTTCT  
TGTTGAAGGGCGCTAGCGATACGAGTCAAGACATCTTTTACCTGACTGTTTACTTCATCC  
AAGTCTGCATCAGCCTTGTGTGGCAGCTTTTAGATTTTCTACTTCTTCTGCCAAAGAT  
TGTCTGATTCTTCTTCATGGATTTCGTTCCAAGAGTTGATTTGCCTTGCTCAAAAGACTT  
TCTACTTCTTCTTGCTATCTGTCGCAGATTATTGGTTGCTATCTACCATGTACTCCTAA  
AACAGGAGAGTTATAATCCAAGATTACAAGGCCTTACAGAAATAAGAAATCCAGATAAGA  
CAATGTTTCGTCCAAGACGCTATTCGCTTCGCACAGCAGCACGGATTCAATATGCTTTAAT  
TTTAAAGTTTAGGTGTCAAGACCTCTTTTGTAGTGTGCCCAAATTTAGAGAAGTAATCAA  
TCAACTAACTTTTATTTTTTCAAACCTTTCAGTAACTGACCTAAAGCTAACTCAATCTG  
TCTTTGTTTCGATAGGCTTGTCTTTGTAGATGCTTCTGCTATCAGATCTAGAAGTTGATCT  
ACTTTTGCCAAGACTGCCTTCTCATCAAAAGTTCCAGGTTGATAGTTGGATTGCAGGGAT  
GGAATCTTGTTTTTCAAAGCCGCTTCATATCCCTTAGTTTGAACCTTGATGTAGTGATTG  
TGGTCGCCACGAGGAATCACAAAACCTTCTGAATCTTCACTTATAATTTCGATTGGCATCA  
AAACCATGACCATCTTCTTCCTCATGGTGGACATGTAGTGACGGATTACTTAATACAGAA  
CTAGAAGAACTTCCTACCTTTTCCGTGTTAGAGTGTGATGGGGGATTGTTAAGAGATGAC  
TTAGGAATATAGTGATAGTGACCCCATGTCTTACTATATAAGCATCACCTGTATCTCTGA  
CAATATCATTAGGGTTAAAGACATAACCATCATCTGCTGCAGAAACACCATTATTTCGGTG  
TCACCGACAAAGATTGACTGAGAGCTGTAGTATTCTCTGATAATTATACTTTTGCAGCTG  
CTAATTCACCTGCCGACAAGTCACTCTCAGGAATGAAATGATAGTGACCACCATGTGGTA  
CTATAGTAGATTGAAATAGAATATGAGCAAATTGATAAGGGGATTTTAAAGTAATTTCTA  
ACAATGATTTAGAACTATGATGTGCTATTCTAAATTCAACTCACTATATATAACCATCA  
TCGGTAGTATAACGTCCCTGTAATTTTGCTACAGATACTTCTGCACTAG

## ORF Predictions:

ORF #	Start	End	Direction	Length
7	948	1160	R	71 aa

[SEQ ID NO: ] 3858118-7 ORF translation from 948-1160,  
direction R  
VIPRGDHNHYIKVQTKGYEAALKNKIPSLQSNYQPGTFDEKAVLAKVDQLLDLIAEASTK  
TSLSNKDRLS\*

Blastp and/or MPSearch Result:

Description:  
unknown

Assembly ID: 3858152  
Assembly Length: 1047bp

[SEQ ID NO: ] 3858152 Strep Assembly -- Assembly  
id#3858152  
ATATTCTCAACCACTGGAGATGGCGCTCGATATCCATGATTAGATTGCGAACGAAAAGAC  
GGGTCAGCTCCAGCTGGCTTTACCAGGACCACGGGAACCAATTCCCCCTGCCTGACGGC  
TGAGCATAATCCCCTGACCAACCAAGCGAGGCAAGAGGTATTTGAGTTGGGCTAGGTGGA  
CTTGGAGCTTCCTTCATGGCTTCGAGCCCGCATGGCAAAGATATCCAAAATCAACTGCA  
TACGGTCAATGACCTTAACACCGAGAACTTCCTCTAGATTGACATTCTGCCTTGGGGTCA  
GACGGTTGTTGACGATGACAGTAGTGATTTCTTCTGCATCCACCATAAGCGCAATCTCTT  
CCAACTTACCAGAGCCGACGAAGGTCTTGGAATCATATTTTTTCACGTTTTTGTCTGTAGC  
TATCTACAACGACTGCCCCTGCCGTTTTTCGCTAAACTAGCCAATTCTTCCATGGAGAGGT  
CAAACTGTCCATACCCTGCAATTCACACCAATCAGCAGGACTCGCTCCTCTTTTTTCT  
CCGTTTCAATCATCTAAAACTCCTCTATCTGGCTTAAATGCGGTCTTGACACCAGAT  
TCTCCAATCTGATAAAAGGTGACCTGCATGCGATTACGGAACCAGGTCAGCTGACGCTTG  
GCAAAACGACGGGTCGCCTGTTTAAGACTCTCACGAGCTTCTCAAAGGTCTGCTCTCCA  
CGGAAATAAGGAAAGAGTTTCCTTATAGCCAATTTCCTTTAGCAGCCTGTACATTAGGGGAA  
TGGTCAAACAGCCACTTGGCCTCATCCAAAAGCCCAGCCTCAAACATCAAATCCACTCGG  
TGGTTGATACGCTCATAAAGTTGACTACGTTTCATCATCCAAGCAGATAATCAGCGGTTCA  
TACAAGATCTCTTGATTTTCCAAATCCTGACCAAAATGGGCAATTCGATGGCACGCATAG  
CACGACGACGATTAAACTGGGGAATCTCAAGGCCTGCTTGCTCCACCAAATGGGCTAATT  
CCTCATCTGAATATGGCTCCAAATTAG

# ORF Predictions:

ORF #	Start	End	Direction	Length
6	546	836	R	97 aa

[SEQ ID NO: ] 3858152-6 ORF translation from 546-836,  
direction R  
VDLMFEAGLLDEAKWLFHDHSPNVQAAKGIGYKELFPYFRGEQTFEEARES LKQATRRFAK

RQLTWFRNRMQVTFYQIGESGVQDRILSQIEEFLDD\*

Blastp and/or MPSearch Result:

Description:

TRNA DELTA(2)-ISOPENTENYL PYROPHOSPHATE TRANSFERASE (EC  
2.5.1.8) (IPP TRANSFERASE) - AGROBACTERIUM TUMEFACIENS.

Assembly ID: 3858258

Assembly Length: 1565bp

[SEQ ID NO: ] 3858258 Strep Assembly -- Assembly  
id#3858258

TCGAATCTGGATATGGAGATTGCCAACCATGTCGTGGTCTTTGGGGGCAAGGAAATCGAT  
GTTCTCTGGAAAATCTGACAGTCGCTGGAAATTAAAGCAAAGAGCTGCCCAGTCTGGAAGT  
TTTCTATTGTCAACCAAGAACGAGAACAGGAAATCAAGGACTATATTGACCAAATCAAAC  
GTGATGGTGATAACCATCGGTGGGGTTGTGGAGACAGTCGTCGGAGGCGTTCCAGTTGGTC  
TTGGTTCCCTATGTCCAATGGGATAGAAAATTGGATGCAAGATTGGCTCAAGCTGTTGTCT  
CTATCAATGCCTTTAAAGGGGTGGAATTTGGTCTTGGCTTTGAGGCTGGTTATCGTAAAG  
GCAGCCAAGTTATGGATGAAATTCTCTGGTCTAAAGAAGACGGTTATACTCGCCGTACCA  
ATAATCTAGGTGGTTTTGAAGGTGGTATGACTAATGGGCAACCCATCGTTGTTCTGTTGGG  
TCATGAAACCCATTCCTACTCTTTATAAACCTCTTATGAGTGTGGATATCGAAACCCACG  
AACCTTACAAGGCAACCGTGGAGAGAAGTGATCCGACTGCTCTTCCAGCTGCAGGAATGG  
TCATGGAAGCAGTTGTAGCAACGGTTCTGGCGCAAGAAATCCTCGAAAAATTCTCATCAG  
ATAATCTTGAGGAACTAAAAGAAGCGGTAGCCAAACACCGAGACTATACAAAGAACTATT  
AAGGAGTTCCTATGGCAAAAACAATCTATATCGCAGGTCTTGGGTTGATTGGAGCCTCTA  
TGGCACTTGGTATCAAACGCGATCATCCAGATTATGAAATTTTAGGTTATAATCGTAGTC  
AAGCTTCGAGAGATATCGCCTTGAAAGAAGGCATGATTGACCGTGCAACGGATGATTTTG  
CTAGTTTTGCTCCTTTGGCAGATGTCATTATCCTCAGCTTGCCAATCAAACAAACTATTG  
CTTTCATTAAGGAGTTGGCCAATTTGGATTTGCGAGAAGGCGTTATTATTTTCAGATGCTG  
GTTTCGACCAAGTCAACCATTGTGGATGCGGCGGAGCAGTATTGGCTGGCAAGTCTGTTC  
GCTTTGTCTGGGGCCCATCCCATGGCTGGTAGTCACAAGACAGGGGCTGCTTCGGCAGATG  
TCAATCTTTTTGAAAATGCCTATTATATCTTTACACCTTCAAGCCTGACAAGTCAGGACA  
CGCTTAAGGAAATGAAGGATCTGCTTTCAGGTCTTCATGCTCGTTTTATCGAGATTGATG  
CCAAGGAGCATGATCGTGTCACTTCTCAGATTAGCCATTTTCCTCATATTTTGGCTTCTA  
GTCTCATGGAGCAGACTGCGGTCTATGCTCAAGAGCATGAGATGGCAAGGCGCTTTGCGG  
CAGGTGGTTTTTCGAGATATGACCCGAATTGCGGAAAGCGAGCCAGGAATGTGGACCTCCA  
TTCTCTTGTCCAATAGCGAGACCATTTCTGGATAGAATTCAGGATTTCAAGGAACGTTTGG

AAGCGATTGGTCAGGCCATTAGTAAGGGAGATGAAGAGCAAATTTGGAACCTTTTAAACC  
AAGCG

ORF Predictions:

ORF #	Start	End	Direction	Length
6	207	722	F	172 aa

[SEQ ID NO: ] 3858258-6 ORF translation from 207-722,  
direction F  
VETVVGGVFVGLGSYVQWDRKLDARLAQAVVSINAFKGVEFGLGFEAGYRKGSQVMDEIL  
WSKEDGYTRRTNNLGGFEGGMTNGQPIVVVRGVMKPIPTLYKPLMSVDIETHEPYKATVER  
SDPTALPAAGMVMEAVVATVLAQEILEKFSSDNLEELKEAVAKHRDYTKNY\*

Blastp and/or MPSearch Result:

Description:

PHOSPHO-2-DEHYDRO-3-DEOXYHEPTONATE ALDOLASE, TYR-SENSITIVE  
(EC 4.1.2.15) (PHOSP HO-2-KETO-3-DEOXYHEPTONATE ALDOLASE)  
(DAHPSYNTHETASE) (3-DEOXY-D-ARABINO-HEP TULOSONATE 7-  
PHOSPHATE SYNTHASE). - BACILLUS SUBTILIS.

Assembly ID: 3858314  
Assembly Length: 983bp

[SEQ ID NO: ] 3858314 Strep Assembly -- Assembly  
id#3858314  
CTGATTAGTTTTCTTCTTTTTTGTCTTTTCAAACCTAGACCACCGAGTAAACCTGCAAGCG  
CAAGCCCAAGGAAACCAATACTTGCCATTGATGTTTGAGTCTCACCAGTATTTGGTAGCA  
TAGCTTTATCCTCTGACATCATCGTATCAGACATCTTGTTAGCAGAAGCAGCCATGTTTT  
CACCTGCCATCGTGTTGGTAGAACTTGTCATGGTGTCAGCAGGCATGCTATCTGTAATAC  
CTGTAGCATGATTGTGATTCATCGGAGTCACGCCAGAACCAGAGTTAGAAGGTGATAATG  
AACCATTTGCTGTGTCTGAAGTTTCTTTAATATTTATCTTAATAGTGAAGTTTTTTAGTTG  
CTACGATGTTGTCCAAGTCTGGTTTACCGTCTTTGTTACCATAGACATTGACTGTAGCGC  
TGTAAGTTTGAGTACCATTTGCTCGGAACCTGGTCAATGAGCGCTTGTTTTTCTTTGCCAG

CTACATTTCCGTCCAAGGCTACTTGATAGAAGTATTGACCTTTGGTCTTCACGTTTTTCAC  
 CTAGTGGAGATAGGGCTGGGTTTTTAGCGTCGCCGTTATCTGACCATGGTGCCTTGTCAG  
 ATGCCTTGAGCAAGAGACGAGTCAACATACCATCACCTGCGAAGAGTTCGTATGGAATCA  
 CATGGTTGACACCTGCTGTGAATGGACCTTCACCCTTGGCTTTTTTCTAGGTAGGCTGCTG  
 GAACATCGATACTGTCTTTAACGTTGTCTGCAACGGCTTTTTGAACTGTTTCTTTAGAAA  
 TTAAACCGTTTTATGTTAATAGTGACTTTTTTAGTTGCTACGATGTTGTCCAAGTCTGGTT  
 TACCGTCTTTGTTACCATAGACATTGACTGTAGCGCTGTAAGTTTGAGTACCATTTGCTC  
 GGAAGTGGTCAATGAGCGCTTGTTTTTCTTTGCCAGCTACATTTCCGTCCCAAGGCTACT  
 TGATAAAATTATTGACCTTTGGC

## ORF Predictions:

ORF #	Start	End	Direction	Length
-----	-----	-----	-----	-----
6	5	661	R	219 aa

[SEQ ID NO: ] 3858314-6 ORF translation from 5-661,  
 direction R

VIPYELFAGDGMLTRLLKASDKAPWSDNGDAKNPALSPLGENVKTKGQYFYQVALDGNV  
 AGKEKQALIDQFRANGTQTYSATVNVYGNKDGKPDLDNIVATKKVTIKINVKETS DTANG  
 SLSPSNSGSGVTPMNHNHATGITDSMPADTMTSSTNTMAGENMAASANKMSDTMMSEDKA  
 MLPNTGETQTSMASIGFLGLALAGLLGGLGLKNKKEEN\*

## Blastp and/or MPSearch Result:

## Description:

Probable cell wall associated protease

Assembly ID: 3858368

Assembly Length: 2138bp

[SEQ ID NO: ] 3858368 Strep Assembly -- Assembly  
 id#3858368

CTTCCAGAACTTCTAAACCAGCCTCCATGATTACTGGGCCAATTCCGTCTCCTAATTAGG  
 AGCTACTATTTTCTTTGCCATAGCCTTCTCCTTTACACACTAGGCATATCGTGGTAAGAA  
 AACTGCGTCCCATCTCACCTGCATTCTTTTTGAACAAAGGTATTAGCGTTTATATAG

GCAATAGCAGAAGCCTTCAACACATCAAAATCAAGCCCTGCTGCATTAAAGATGGTTTCT  
 GTATCTCTGTTTTCAACAGTGACCAAACCCGATCCTGGGCATCGATTCCATCTGTTACC  
 GCATTGATAGTGTAGGACACCAAACGAACAGATTGGTTAAAGAACTTATCGATAGCGTTA  
 AAGATTGCTTCAACGGAACCTTGCCCTGTGCGATTAAATTCGACTTTCTCACCATCCATA  
 TTGGCTAGGCTAACGAGCGCTTCAATGTCAATTATCTGCATGAGTTTGAAGTTGTAAATCA  
 TCAAAGTGGAAGCCTTCTGGATTTTCAACCATGGTTCCAGCTACCAAAGCTCGAGTATCT  
 GCATCTGTGATTTCTTACTTCTTATCGGCCAGTGCCTTGAACCTAGCAAAGAATGGTTTG  
 ATATCCTCTTCTGTAAAATCTAAGGCCAATTCTCTCAGTTTCTCAACAAAAGCATGGCGA  
 CCAGATAATTTTCCAAGCGGAATCTTAACACCAACCAATTCAGGTGTGATGATCTCATAA  
 GTGAGAGGATTTTTAAGGACTCCATCTTGGTGAATACCAGATTCTGGGGAGAAGGTATTG  
 CCACCAACGACGGCTTTGTTTTTAGGAACTGGAATACCAGAGAAGCGAGAAACCATTCT  
 GACGTATTGATGGTCTCATTTAGGACAATACTGGTTTCTACTTGGTAGTAATCTTGGCGA  
 ATATTGAGAGCCAATCGCAATCTCTTCCAAAGCAGCATTTCCAGCTCGCTCCCTAATACC  
 ATTGATAGTCTCTTCAACACGTCTCTGCACCATTTCTTGACAGCAGCAAGGCTATTTGCCAC  
 TGCCATTTCCGAGGTCATCATGACAGTGAGGCGAATAGATGATCTGACGATCCGTCTTGAC  
 ATTCTCAATCAGGTATTTGAAGATGGCACCACATTCCTCTGGTGTGGTAAATCCTATATT  
 TTCTGAAAATTTCTTCAGTAAAGAATATTTAGCTAATTGAAAGTTCATGAAAATTATTAA  
 AATATTTTCATTTTTTAGAGGTTAAGTTCCAACCTTTTTTCTATCAATTCCAGTACTTCTTC  
 ATCTGATAAAGTATCATCAAGGGACACACTAATCCAGTAGCGCTTGCTCATATGGAAGGC  
 TGGATAAATCCCTTTTTGTGAAAGCAAATTAGCTACTTGGTCATGCTTGAGGTTGACTGC  
 TTCCACTTGTCTTCTCTGCCCTTTTCCAGCTTATTCCAAGAGATTTTCATCAAGACGGC  
 ATACCACTTTTGATTGCCTTCATGGCGCAATACAGCTGTATCAGGCGATTTTCCCACAG  
 ATACTCCAACCTGGTTTTCCATACTTTTCCTGAACTTGAGTCATGATACGCTTAGTCTGATG  
 ACAGATAAAATCTTGCACATCAAAACAAGCCTTCCGAATCTGGTAAAGAATCTCCAGACA  
 AGCCTCACGGACATTTCCGACAAAATTCCTTCATGCTTTCCATATGAACGTGAGGATAA  
 AGGTCACCAGTCTCTTGGTCAAAGACTGGAAAGTTCAACATTATCAGCAGTGATGGACAC  
 AGTCATGACAAAGTCACCTTGCAAAATCTGGCAACTATATGTCCAGAATTCCTTATTTTC  
 CTATAAAAACCATAATCATGAAGCCTTTTTCTTGGATTAAATTGATAGGATTTAAAAATT  
 TCAAACATAAGTTGAAAACCTGCTACCCAAGGCTTAGCAGTTCCTTTCCTATTTTTTAAAA  
 AACACCTTAGTACCATGCAATTGTGTTACCCCCACCTGGTCAATAAAGGTTTGACGGTT  
 GTCAAGGTCAATCCCCCACCTGGTAGAATTTCAATTTTACCTTTAGCGTACTCCAAAAT  
 TCTGTGATAGTGAACAAAACGTTTTTCTAAGGAGTCGCCAGACACACCAGCACGAGTTAG  
 GATACGAGTGACACCGGCTTGACTGAGCCAGTCAATAG

## ORF Predictions:

ORF #	Start	End	Direction	Length
9	1207	1578	R	124 aa

[SEQ ID NO: ] 3858368-9 ORF translation from 1207-1578,  
direction R  
VQDFICHQTKRIMTQVQEKYGNQLEYLWEKSPDTAVLRHEGNQKWYAVLMKISWNKLEKG  
REGQVEAVNLKHDQVANLLSQKGIYPAFHMSKRYWISVSLDDTLSDEEVLELIEKSWNLT  
SKK\*

Blastp and/or MPSearch Result:

Description:  
unknown

Assembly ID: 3858556  
Assembly Length: 735bp

[SEQ ID NO: ] 3858556 Strep Assembly -- Assembly  
id#3858556  
ACAGCTCACATCACTGTAGCTGTTGCAGAAAAATAAGGAGGTAAAATCGTGGGTCAAAAA  
GTACATCCAATTGGTATGCGTGTCGGCATCATCCGTGATTGGGATGCCAAATGGTATGCT  
GAAAAAGAATACGCGGATTACCTTCATGAAGATCTTGCAATCCGTAAATTCGTTCAAAAA  
GAACTTGCTGACGCAGCAGTTTCAACTATTGAAGTCGAACGCGCAGTAAACAAAGTTAAC  
GTTTCACTTCACACTGCTAAACCAGGTATGGTTATCGGTAAAGGTGGTGCTAACGTTGAT  
GCACTCCGTGCAAAACTTAACAAATTGACTGGAAAACAAGTACACATCAACATCATCGAA  
ATCAAACAACCTGATTTGGATGCTCACCTTGTAGGTGAAGGAATTGCTCGTCAATTGGAG  
CAACGTGTTGCTTTCCGTGCTGCACAAAAACAAGCAATCCAACGTGCAATGCGTGCTGGA  
GCTAAAGGAATCAAACTCAAGTATCAGGTCGTTTGAACGGTGCAGATATCGCCCGTGCT  
GAAGGCTACTCTGAAGGAAGTGTTCGCTTCACACACTTCGTGCAGATATCGATTACGCT  
TGGAAGAAGCAGATACTACATACGGTAACTTGGTGTTAAAGTATGGATCTACCGTGGT  
GAAGTCCTCCCAGCTCGTAAAAACACTAAAGGAGGTAAATAACCAATGTTAGTACCTAAA  
CGTGTTAAACACCGT

ORF Predictions:

ORF #	Start	End	Direction	Length
6	49	702	F	218 aa

[SEQ ID NO: ] 3858556-6 ORF translation from 49-702,  
direction F  
VGQKVHPIGMRVGIIRDWDKWAYAEKEYADY LHEDLAIRKFVQKELADAAVSTIEVERAV  
NKVNVSLHTAKPGMVIGKGGANVDALRAKLNKLTGKQVHINIIEIKQPDLD AHLVGE GIA  
RQLEQRVAFRR AQKQAIQRAMRAGAKGIKTQVSGRLNGADIARAEGYSEGTVPLHTLRAD  
IDYAWEEADTTYGKLG VKVWIYRGEVLPARKNTKGGK\*

Blastp and/or MPSearch Result:

Description:

30S RIBOSOMAL PROTEIN S3 (BS2). - BACILLUS  
STEAROTHERMOPHILUS.

Assembly ID: 3858562  
Assembly Length: 1965bp

[SEQ ID NO: ] 3858562 Strep Assembly -- Assembly  
id#3858562  
CTGTGTGATTCCATTATTTGTCAAATACTTTTTAGTTTCAGCAATAACGACTTGCGACA  
AGACCAAGAGGGCAATCNANTTTGGCAGAGCCATCAAGGCGTTAACGATATCTGCGATAA  
TCCAGACCATNTCCAACCTCGATAAATCCTCCTAACAAGACCATGAGCACAAAAACACNC  
GGTAGAGCCAGATAAAGCGAACCCCAAAGAGGAAC TCAAAACAGCGTTCTTCCGTAATAG  
TTCCAACCTAGAATCGTTGTAAAGGCAAAAAGCACAAAGGAAGATGGTCAAGAAGGCAGGC  
CCAAAGTGTGAAAAGACTGTTGAGAAAGCTGACTGAGTCAAGGCAACCCCATTCAGTCA  
CCTCTCCAAACTCCAGTTACCAAGATGGTCAAACCAGTTAGAGTACAAATGATGAGGGTA  
TCAATAAAGGTTCTGTCTATGGAAATCAAACCTTGCTCTACTGGTTCATTTGTCTTGGA  
GCTGCAGCTGCAATAGGAGCAGAACCCAGACCAGATTCGTTTGAAAACACACCACGCGCC  
ACACCATTTTGAATAGCCATCCGAACGCTAGCACCAGCAAATCCACCTACCGCAGCAAGG  
GGACTAAAAGCTGAGGTAAAGACTAAAGCGATTGTGCCAGGGATTTTCCGATATTAAAG  
AAAATAACTGTAAGAGTTCCTAAGATATAAATGATGGCCATAAAAGGAACAACAGTAGTT  
GAAACCTTAGAAATAGACTTGAGTCCACCAAAGACTGCAATCGCTACAAAGACAGACAAG  
ACGAGAGCTGTGATGGCTGGCGAAATCGTCGTTGTATTTTGATAGATTCTGTAATCGAG  
TTGACTTGGGTGAAGGTTCCGATTTCCCAAGAGAGCAACCAATACTCCTGCTACTGCAAAC  
AAAACAGCAAGTGGTCGCCACTTTTCTCCCATCCCTAGAAGGATATAATGCATGGGACCT  
CCCGCTACTGCACCATGGTCGTCCTTGGTGCGGTATTTGATGGCCAAGAGTCCTTCCGCA  
TACTTGGTAGCCATTCCAAAGAAAGCCGCCATCCACATCCAAAATAGAGCTCCTGGTCCA  
CCAACCTTGATAGCCGTCGCCAACTCCCTAATGAATATTTCCCTGTTTCCCAACCAAGTTT  
GAATGCCCCAAGGGCCTGTTACACAAGAAGCTGTAAAACTGGATACATCACCATGTCCCTT



ATCCTGGATAAAAAATAAGCTGAAAGGCCTTGGGCAGACGCAAAACCTGCAAGAGTCCTAG  
 CCGCATGGTTAGGTAAATCCCTGTTCCGACCAATAAATCAAGAGGGGCGGTCCCCAAGCA  
 AAAGCATCGATTGATTAAAGCAATTCTAACATTTCCCTTCTCCTATCGTTTCAACCCCAA  
 AGAAAGAGCACATGCAAGATACATGTACTCTGGAATGCTTAGATAAATGCTAAAAAGCGG  
 TCTATCCTAGCTCTGTCCTTTTACCTGAGAGTTTGAGCAGTTGCCTGCCTTGCCCCCTCG  
 GTGCCTTTACGGTCTCTCCAGAGTTCCGTCCATTTACAGTCATGGAAAATCAAACGATTC  
 CCCACTTCTATTAACTTCATTCGGTGTGGTATTTAATTGATTCTAATTTACAAAAAA  
 TGTGGCTTTTGTCAATGTGTTTATTAGTAAAAATTAGTTCAACAGTTTTTACTTTATAA  
 AGTCCAGAATACTGCTATCCTTTAAAAGTGACAATAGTCGCACCACTGCCTCCAGCATTT  
 TGTGGGGCATAGCCGAACTCTTGACATGTTTGTCTCTTTGCAAGTTATCTGGTAACTCC  
 TTCACGGGATGACTCCTGTTCCGATACCATGGGATGACATCAACTCGAAGCCCTTATATT  
 GTTAACCAAAGCTTGGTGAATGAAGGTATCTAGCCCATTCATGGCTTCTTCATAGCGCT  
 TGCCTCGAAGATTACAGTCTAGCTTGAGTCCTCGCCCAGAAGTTTCG

## ORF Predictions:

ORF #	Start	End	Direction	Length
6	14	178	R	55 aa

[SEQ ID NO: ] 3858562-6 ORF translation from 14-178,  
 direction R  
 VVFLVMVLLGGFIELXMVWIIADIVNALMALPXXIALLVLSQVVIAETKKYFDK\*

## Blastp and/or MPSearch Result:

## Description:

D-alanine permease (dagA) homolog - Haemophilus influenzae  
 (strain Rd KW20)

Assembly ID: 3858656

Assembly Length: 1187bp

[SEQ ID NO: ] 3858656 Strep Assembly -- Assembly  
 id#3858656  
 ACGTTTGTCAATTAATTATGAACTAAGAGAAAAATTGTTTCAGGAAGCAGTAAAATTGGT

GTCAGATAATGAAACAATAATGATAGAATCTGGATCGACCTGTGCTTTACTTGCTGAGGA  
 AATTTGCAAGCAAAAAAGAAATGTTACGATTGTAACAAATTCGTTTTTTATAGCAAATTT  
 TGTGAGAGCTTATGATTCATGTCGTGTTATTGTTCTTGGTGGTGAGTTTCAGAAAGATTC  
 ACAGGTGACTGTAGGACCTTTATTAAAAGAAATGATACAGACTTTTCATGTGTGTCAAGC  
 TTTTGTGTTGGGACAGATGGTTACGATAAAGAGATGGGCTTTACCGGAAAAGATTTAATGCG  
 CAGTGAGGTAGTTCAATATATTTTCAGCAGTGTCTCGGATAAAGTCATTGTCTTAAGTCAAGTCTATGAAGT  
 AAGTAAATTTGATAAAGAGGTACAGTAAGAAGATTTGCTTTAAGTCAAGTCTATGAAGT  
 AATAACAGACGAAAAACTTTCTAAACAAAATATAGCTACATTAGAAAATGCTGGGATAAT  
 GGTAAAGGTAGTTTCGTAAGAGGTAAAGTGTATGAATCAAGATAGGAATAAACTGCTTTC  
 TAAAAATTGCTTATCTGTATTATATTGAAAACCTAAATCAGTCACAAATAGCAGCAAAATTT  
 AGGAATTTATAGAACCTCTATTAGTAGAATGTTAACAGAAGCAAGGAATGTAGGAATTGT  
 TAAAAATTGAAATAGAGAATTTTGATACCAATATGTTTAAAGTTGGAAAATTATGTAAAAGA  
 AAAATACAGTTTGGAAAGTTTAGAAATTATTCCAAATGAATTTGATGATACTCCAACAAT  
 TTTATCTGAAAGAATTTCTCAAGTTGCAGCAGGCGTCCTTAGGAATCTAATTGATGATAA  
 TATGAAAATTGGCTTTTCTTGGGGGAAAAGTTTAAAGTAATTTAGTAGATTTAATTCACAG  
 TAAAGTGTCCGAAATGTTCACTTCTATCCTCTAGCAGGTGGTCCTAGTCACATACACGC  
 TAAATACCATGTGAATACACTGATTTATGAAATGTCTAGAAAATTTTCATGGAGAGTGTAC  
 ATTTATGAATGCAACGATTGTGCAAGAAAATAAATTGTTAGCAGATGGTATTTTGCAATC  
 AAGATATTTTGAAAATTTGAAAAATAGTTGGAAAGATTTAGATATAG

## ORF Predictions:

ORF #	Start	End	Direction	Length
6	245	559	F	105 aa

[SEQ ID NO: ] 3858656-6 ORF translation from 245-559,  
 direction F

VTVGPLLKEMIQTTFHVCQAFVGTGDGYDKEMGFTGKDLMRSEVVQYISAVSDKVIVLTDSS  
 KFDKRGTVRRFALSQVYEVIITDEKLSKQNIATLENAGIMVKVVS\*

## Blastp and/or MPSearch Result:

Description:  
 unknown

Assembly ID: 3859118

Assembly Length: 843bp

[SEQ ID NO:     ]     3859118 Strep Assembly -- Assembly  
id#3859118  
AGCTATTGCAGGAACCAAGATNATGATTTTGGTACGTGGAGTTTGGTATTTATTNTACC  
TCAAATCCTNGCAAATATGATTGGTTTGGACTACGATTTCTTGGTTAATCAATCAAATTAT  
TACTTATGGGGTTATTGCGGCGGTTGTTATCTTCTCTCCAGAGATTCGGACTGGTTTTGG  
AACGTTTGGGAAGAGCGACAGATTTCTTTTCCAATGCCCCCTATTAGTGCTGAGGAACAGA  
TGATTTCGTGCCTTTGTTAAGTCTGTCTGAATACATGAGTCCTCGTAAAATCGGGGCCTTGG  
TTGCCTATTTCAGCGTGTACCGTACCTTGCAGGAGTATATTTTCGACAGGAATCCCCCTGGA  
TGCTAAGATTTCTGCAGAACTTCTCATTAACATTTTTATTCCCAACACTCCCCCTACATGA  
CGGTGCGGTGATTATCAAAGAAGAACGTATCGCTGTGACGTCTGCCTATCTGCCCTTGAC  
AAAAACACAGGTATTTCCAAGGAATTTGGGACCAGACACCGGGCGGCTATCGGTTTATC  
AGAAGTCTCAGATGCCTTGACTTTTGTCTGATCAGAGGAAACGGGAGGAATTTTGATAAC  
CTATAATGGAAGGTTTAAGCACAACTAACACTTGATGAATTTGAAACAGAATTACGTTG  
AAATCTTACTTCCAAAAGAGGAAGTGGGTCCTTAGTTTTAAAGAAACGAATGGCTAGGAG  
GAATGGAAACATGAAAAAAAAATAGTTTATATATCATATCCTCACTCCTTTTTTGCTTGT  
GTCTTATTTGTCTATGCTACGGCGACGAATTTTCAAACAGTACCAGTGCTAGGCAGGTT  
AAA

#### ORF Predictions:

ORF #	Start	End	Direction	Length
6	314	661	F	116 aa

[SEQ ID NO:     ]     3859118-6 ORF translation from 314-661,  
direction F  
VYRTLQEYISTGIPLDAKISAE LLINIFIPNTPLHDGAVIIKEERIAVTSAYLPLTKNTG  
ISKEFGTRHRAAIGLSEVSDALTFVSEETGGISITYNGRFRKHNLTLEDEFETELR\*

Blastp and/or MPSearch Result:

Description:  
unknown

Assembly ID: 3860084  
 Assembly Length: 710bp

[SEQ ID NO: ] 3860084 Strep Assembly -- Assembly  
 id#3860084

ATCGAATTAGTTGTTGGGTTGATTACCTTCCAAGAAAACTAGCCCTTCTAGCCTTACTA  
 GGAGCTGGTTTGGTTTACTAGTCTTGTATTTGCCTTATCAGGTAAAACGTCAGATGCAG  
 GACTAACATTGCTGATACGACACTAAAAAAGAAGTTGAGTTCAGTTTGTCTCAGCTTCTT  
 TTTTGTTACTACAGGATAATGGTTGGTCCGTAGAGACTTATACTCTTCGAAAATCTCTTC  
 AAACCACGTCAGCGTCGCCTTACCGTACTCAAGTACAGCTTGCGGCTAGCTTCCTAGTTT  
 GCTCTTTGATTCTCATTGAGTATTAAGTTGGTCTTGACTGGGTCAAAGTGGAAGCGGTCA  
 TAGGCCCCGCCAAGCGGCGCGAGTTGGAGCATCTGGATCAAGAGCGCTGAGTCCCATGAGA  
 AGACTGGAAGTCTGGTAAAATTTTCTAGTTCAATCAAGAATCGATTATCCACTGTTTCA  
 GCCTTGCGCTAGAAAACCAAGAATAGAATTTAATTCGATCCCTGAAAGCGGACGTCGTCAG  
 CGCTTGCGCTGTTTGCATGCTTGGTAGGCTTTGTTTAAGTCAGTAATCAAAGTATGAGCTC  
 TTTTGATGGGGTCTGTATCTGTCATGGGAATGCCTCCTTTAATCTGGGTGCCAGTCTTAC  
 TTCTGGCAACTGTGTTTTGATACTGTTAGTTTATCAGCTTTTAATTCGAT

ORF Predictions:

ORF #	Start	End	Direction	Length
6	294	473	R	60 aa

[SEQ ID NO: ] 3860084-6 ORF translation from 294-473,  
 direction R  
 VDNRFLEIELEKFYQTSSLLMGLSALDPDAPTRAARAYDRFHFDPVKTKLILNENQRAN\*

Blastp and/or MPSearch Result:

Description:  
 unknown

Assembly ID: 3860172  
 Assembly Length: 1975bp

[SEQ ID NO: ] 3860172 Strep Assembly -- Assembly  
id#3860172

CTTGATCTTGACCGATGACACGTTTGTGTCAGTTCAGCTTCCAAGTTTAAGTATTTCTTG  
CATCAGTCTGAGTCAGTTTTTGAACGGGGATACCTGACAAGCGACTCAAGGTGGTCAAAA  
TATCAGACTCTGTCACCAAGTCTTTATAGACAGGCACTTCCTCTTCTTTTTCGATTAGCT  
GGGCTGCCTGTTTCCACTTGCCATCCATCAAGGCCTTGTCAGCTGGACTCAAGTCAGAAT  
CGTCTGCTTTTACATGCTTTGATTTATTTTGCAGTGTGCTGCCGCCTCATCCAAGAGAT  
CGATAGCAGAGTCTGGCAAGTGACGACTGGTTAAATAACGATGAGCCATCTTAACCGCTG  
TTTCAACCGCTTCATCTGTGATTTGTACACGGTGATGTTTCTCATAAGTCGCCTTCAAAC  
CTTGTAATAAGTATCATACTATCTGCCACACTTGGTTCTTCAATCGTCACTTTAGCGAAAC  
GACGAGAAAGTGCCGCATCTTTTTCGATATGTTTTTGATATTCTTCCTGAGTGGTGGCAC  
CAACCGTTCTCAAAGTTCCACGCGCCAAGGCTGGTTTCAAGATATTGGCCGCATCCAGAG  
TCGAATCAATTCGGCTACCAGAACCCATGATGGTGTGGAGTTCATCGATAAAGAGGATGA  
CTTGCCCATCTTCTTCAATATCCTTGATGATATTATTCATGCGTTCTTCAAAGTCACCAC  
GGAAGCGTGTCCCTGCAACGACATTCATCAAATCAAGTTCTAACACGCGCATCTTAGCCA  
TTTCCGCAGGCACGTCACCACTGGCAATACGCTGGGCAAGACCAAGCGCCAGAGCTGTTT  
TCCCGACACCAGCATCCCCAACCAAGACAGGGTTGTTCTTAGTCTTCCGGCTTAAGATTT  
GAATCATACGTGAGATTTCTTGTCCCGACCGATGACTGGTTCTAACTTGCCAGAACGCG  
CTTGCTCTGTCAAATCATGCGTATAGTCTCAAGACCACCACTAGGAGTCTGCGGCATGC  
CCATCATATTGGCCATAGAATTTTGCTTGTGCTACTGTACGATGGCGTTGGCGCAAAG  
CCTTGAGATCTTCACGAGTCCAGCCTGCCGTTCTTCTAAATTTTCGACGAAGAGCAGCAA  
TCTTGACCTGATCTTTCTTGTCTTCATAAGAAAAACCAGCCCTCTCCAAGATACGAGTCG  
CCAAGGCATTGCCATCATGCAAAATCGCATAGAGGACGTGCTCTGTCCCTAGCACCTTAG  
CATGGACCACTGACACTACATACTCTGCTTCGTCAAAAAGAACCTGCAAACGACGGGAGA  
ACGGCAATTCCGTAAAGGTTTCATCCTGGCTATAGTCCGTTTCAGTCAGTTCCAAAGCCA  
CCTCTTCTAAACGGTCCATCTCATAACGGATAATCATTTAAAGTTGCCCCCTGCTACACTAT  
AACTGTGATTAGACATGGCAATCAACAAGTGCCAAGACTCTAGATAACGAGGCTCCAAAA  
TGTCCAGCAACCATGTAGGCACTTTTCGATACATTCAATGCTTTTGAATAGTTCATC  
TTACTTCCCTTTTCTATCTACCTCTTGTATGACCTGACGTAGCATGTTTGCTCGAACAAC  
TGGAGCTTCTTCTCCTAAACGCGATCCAAAGCTACTGATTCTAGCAAATTCATCTCCTG  
CTTGGTCATCAATTCCCTGCTCAACCAAAAGCTGGAGAATATCCTCATAAAATTCGATGAC  
TGACTCGCTCACCAATCGAGTAAAGCAGCTCCCGGAACATTTTCATGATGACTAGAAAAC  
CAATCCGTCTTATACGAATGTAGCCTCCACCACCACGCTTACTTTCAACCAAGTAGCCTC  
TACTTTCCGTAAAGCGTGTCTTGATCACGTAGTTAATCTGACTAGGAACAACCTGAAAGG  
TATCTGCCAACTGACTCCGTTGCAACTCCACGATACCAGATTGATCTAAAATCGC

#### ORF Predictions:

ORF #	Start	End	Direction	Length
8	1724	1888	R	55 aa

[SEQ ID NO: ] 3860172-8 ORF translation from 1724-1888,  
direction R  
VIKTRFTESRGYLVESKRGGGGYIRIGRIEFSSHHEMFRELLYSIGERVSHRNL\*

Blastp and/or MPSearch Result:

Description:  
unknown

Assembly ID: 3860242  
Assembly Length: 1592bp

[SEQ ID NO: ] 3860242 Strep Assembly -- Assembly  
id#3860242

GGCCCATTAGTGGTAACTCTTTTTGCAGCCTTAACAGGCGCATTGATTTTTCTGGCCAC  
GAATCTGGGATTTATTATTTTAAACAGTAAGAGGAAATTATGACTTTTAAATCAGGCTTT  
GTAGCCATTTTAGGACGTCCCAATGTTGGGAAGTCAACCTTTTAAATCACGTTATGGGG  
CAAAAGATTGCCATCATGAGTGACAAGGCGCAGACAACGCGCAATAAAATCATGGGAATT  
TACACGACTGATAAGGAGCAAATTGTCTTTATCGACACACCAGGGATTCACAAACCTAAA  
ACAGCTCTCGGAGATTTTCATGGTTGAGTCTGCCTACAGTACCCTTCGCGAAGTGGACACT  
GTTCTTTTCATGGTGCCTGCTGATGAAGCGCGTGGTAAGGGGGACGATATGATTATCGAG  
CGTCTCAAGGCTGCCAAGGTTCCCTGTGATTTTGGTGGTGAATAAAATCGATAAGGTCCAT  
CCAGACCAGCTCTTGTCTCAGATTGATGACTTCCGTAATCAAATGGACTTTAATCGGAAA  
TTGTTCCAATCTCAGCCCTTCAGGGAAATAACGTGTCTCGTCTAGTGGATATTTTGAGTG  
AAAATCTGGATGAAGGTTTCCAATATTTCCCGTCTGATCAAATCACAGACCATCCAGAAC  
GTTTCTTAGTTTCAGAAATGGTTCGCGAGAAAGTCTTGACCTAACTCGTGAAGAGATTC  
CGCATTCTGTAGCAGTAGTTGTTGACTCTATGAAACGAGACGAAGAGACAGACAAGGTTT  
ACATCCGTGCAACCATCATGGTCGAGCGCGATAGCCAAAAAGGGATTATCATCGGTAAAG  
GTGGCGCTATGCTTAAGAAAATCGGTAGCATGGCCCGTCGTGATATCGAACTCATGCTAG  
GAGACAAGGTCTTCCTAGAAACCTGGGTCAAGGTCAAGAAAACTGGCGCGATAAAAAGC  
TAGATTTGGCTGACTTGGGCTATAATGAAAGAGAATACTAAGTAGAGGTAGGCTCATGCC  
TGCTTCTTGTTTTTACAGAAGGAGGACTTATGCCTGAATTACCTGAGGTGAAACCGTTT  
GTCGTAGCTTAGAAAAATTGATTATAGGAAAGAAGATTTTCGAGTATAGAAATTTCGCTACC  
CCAAGATGATTAAGACGGATTTGGAAGAGTTTCAAAGGGAATTGCCTAGTCAGATTATCG  
AGTCAATGGGACGTGCTGGAAAAATATTTGCTTTTCTGCCTGACAGACAAGGTCTTGATTT  
CCCATTTGCGGATGGAGGGCAAGTATTTTTATTATCCAGACCAAGTGCCTGAACGCAAGC

ATGCCCATGTTTTCTTCCGGTTTGAAGATGGGGGCACGCTTGTTTATGAGGATGTACGCA  
 AGTTTGGAAACCATGGAACCTCTTGGTGCCTGACCTTTTAGACGCCTACTTTATTTCTAAAA  
 AATTAGGTCCTGAACCAAGCGAACAAGACTTTGATTTACAGGTCTTCAAGCTGCCCTTG  
 CCAAGTCCAAAAAGCCTATCAAATCCCATCTCCTAGACCAGACCTTGGTAGCTGGACTTG  
 GCAATATCTATGTGGATGAGTTCTCTGGCGAG

## ORF Predictions:

ORF #	Start	End	Direction	Length
7	573	1001	F	143 aa

[SEQ ID NO: ] 3860242-7 ORF translation from 573-1001,  
 direction F  
 VSRLVDILSENLDGEFQYFSPDQITDHPERFLVSEMVREKVLHLTREEIPHSVAVVVDSM  
 KRDEETDKVHIRATIMVERDSQKGIIIGKGGAMLKKIGSMARRDIELMLGDKVFLETWVK  
 VKKNWRDKKLDLADLGYNERY\*

## Blastp and/or MPSearch Result:

## Description:

GTP-BINDING PROTEIN ERA HOMOLOG. - STREPTOCOCCUS MUTANS.

Assembly ID: 3860282

Assembly Length: 1604bp

[SEQ ID NO: ] 3860282 Strep Assembly -- Assembly  
 id#3860282  
 TCATCAAAAGCAGTTAACGAATTGTGAGCGTGTGTTATGAGAAATCATGAAAGTACGGAC  
 CGATACATATAAAAAGGATTTAACTATGGAAGAATTCTCTGTATTGGTTGTGGAGCAACC  
 ATTCAGACGACAGATAAAGCTGGTCTTGGTTTTACCCCCAGTCGGCACTTGAAAAAGGT  
 TTGGGAGACTGGCGAAGTCTATTGCCAACGCTGTTCCGTCTCCGCCACTACAATGAATCA  
 CAGATGTCCAGTTGACGAACGATGATTTCCCTCAAGCTCTTGACGAGGTGGGAGACAGTG  
 ATGCTTTAGTGGTCAATGTCATTGATATCTTTGATTTTAATGGATCTGTCATCCCAGGTT  
 TACCACGTTTCGTCTCGGGCAATGATGTCCTCTTGGTAGGAAATAAAAAAGATATCCTTC  
 CTAAGTCAGTTAAGTCTGGTAAGATTAGCCAGTGGCTCATGAAACGTGCCCATGAAGAAG

GTCTTCGTCCAGTCGATGTGGTCCTAACTTCAGCACAAAATAAACATGCCATTAAGGAAG  
 TCATTGACAAGATTGAACACTACCGTAAGGGCCGCGATGTCTATGTGGTCGGTGTGACCA  
 ACGTTGGAAAATCAACTCTAATCAATGCTATTATCCAAGAAATCACGGGTGATCAGAATG  
 TCATCACTACTTTCACGCTTCCCAGGGACAACCTTGGACAAAATAGAGATTCCGCTTGACG  
 ACGGATCTTATATTTACGATACGCCGGGAATTATCCACCGTCACCAGATGGCTCACTACT  
 TGACGGCCAAAACCTCAAGTATGTCAGTCCTAAAAAGGAAATCAAGCCTAAGACCTATC  
 AGCTTAATCCTGAGCAAACCCTATTTTTAGGTGGTTTGGGACGCTTTGACTTTATAGCAG  
 GAGAAAAGCAAGGATTTACTGCTTCTTTGATAATGAACTCAAACCTCCATCGTAGCAAGC  
 TTGAAGGAGCTAGTGCTTTCTACGATAAGCACCTGGGAACCTCTTCTGACACCACCAAATA  
 GCAAGGAAAAAGAAGATTTCCCAAGGCTAGTCCAGCATGTCTTTACCATTAAGATAAGA  
 CAGACCTAGTCATCTCAGGCCTAGGATGGATTTCGTGTAACAGGCACAGCAAAAGTCGCCG  
 TCTGGGCACCAGAAGGCGTCGCCGTCGTACACGAAAAGCAATTATTTAAGCACAGAAAG  
 GAAAGGGTTGTCTGAATTTGGGCGAGCAAGGCGAGCCCCATAGAGAATACTTTTCGCTGT  
 GGTGTAAGTTGGTACAAGTGATTGTACCAACTGCGGAAAATTTGAGACCTTAGGCTCAA  
 TTTTAGTCATGAAAGTCCGAAGGACTTTGCTGACGTCCGTCACCACTTCAGAAAAGTATA  
 AAAAGAACTCTTTTAAAGAAATTATGTCATTAACATCAAAACAACGTGCCTTCCTCAAC  
 AGCCAGGCACACACCCTCAAACCTATCATCAAATCGGGAAAAATGGACTCAACGACCAA  
 ATCAAAACCAGCGTCCGTCAAGCTCTTGATGCCCGTTGAATTAATCAAGGTTACTCCCC  
 TTTACAAAACACAGATTGAAAACATCCCGGACGAATGTAATTTCG

## ORF Predictions:

ORF #	Start	End	Direction	Length
6	288	1190	F	301 aa

[SEQ ID NO: ] 3860282-6 ORF translation from 288-1190,  
 direction F

VGDS DALV VNV IDIFDFNGSVIPGLPRFVSGNDVLLVGNKKDILPKSVKSGKISQWLMKR  
 AHEEGLRPVDVVL TSAQNKHAIKEVIDKIEHYRKGRDVYVVGVTNVGKSTLINAI IQEIT  
 GDQNVITTSRFP GTTLDKIEIPLDDGSYIYDTPGIIHRHQMAHYLTAKNLKYVSPKKEIK  
 PKTYQLNPEQTLFLGGLGRFDFIAGEKQGFTAFFDNELKLHRSKLEGASAFYDKHLGTLL  
 TPPNSKEKEDFRLVQHVF TIKDKTDLVISGLGWIRVTGTAKVAVWAPEGVAVVTRKAI I  
 \*

## Blastp and/or MPSearch Result:

## Description:

unknown



Assembly ID: 3860296  
Assembly Length: 2025bp

[SEQ ID NO: ] 3860296 Strep Assembly -- Assembly  
id#3860296

CCGTAATGGGTCGTAACCTTGCCCTTAATATTGAATCACGTGGTTACACAATTGCTATCT  
ACAACCGTAGTAAAGAAAAAACGGAAGATGTGATTGCTTGCCATCCTGAAAAGAACTTTG  
TACCAAGCTATGACGTTGAAAGTTTTGTAACTCAATCGAAAAACCTCGTCGTATCATGC  
TGATGGTTCAAGCTGGACCTGGTACAGATGCTACTATCCAAGCCCTTCTTCCACACCTTG  
ACAAGGGTGATATCTTGATTGACGGTGGAATACTTTCTACAAAGATACCATCCGTCGTA  
ATGAAGAATTGGCAAACCTCAGGTATCAACTTTATCGGTACTGGAGTTTCTGGTGGTGAAA  
AAGGTGCCCTTGAAGGTCCTTCTATCATGCCTGGTGGACAAAAAGAGGCCTACGAATTGG  
TTGCGGATGTTCTTGAAGAAATCTCAGCTAAAGCACCAGAAGATGGCAAGCCATGTGTGA  
CTTACATCGGTCCTGATGGAGCTGGTCACTATGTGAAAATGGTTTACAATGGTATTGAGT  
ACGGTGATATGCAATTGATCGCAGAAAGCTATGACTTGATGCAACACTTGCTAGGCCTTT  
CTGCAGAGGATATGGCTGAAATCTTTACTGAGTGGAACAAGGGTGAATTAGACAGCTACT  
TGATCGAAATCACAGCTGATATCTTGAGCCGTAAAGACGATGAAGGCCAAGATGGACCAA  
TCGTAGACTACATCCTTGATGCTGCAGGTAACAAGGGAACCTGGTAAATGGACGAGCCAAT  
CATCTCTTGACCTTGGTGTACCATTGTCACTGATTACTGAGTCAGTGTTTGCACGCTACA  
TTTCAACTTACAAAGAAGAACGTGTACATGCTAGCAAGGTGCTTCCAAAACCAGCTGCCT  
TCAACTTTGAAGGAGACAAGGCTGAATTGATTGAAAAAATCCGTCAAGCCCTTTACTTCT  
CAAAAATCATTTTCATACGCACAAGGATTTGCTCAATTGCGTGCTAGCCTCTAAAGAAAACA  
ACTGGAACCTTGCCATTTGCAGATATCGCATCTATCTGGCGTGATGGCTGTATCATCCGTT  
CTCGTTTCTTGCAAAAGATTACAGATGCTTACAACCGCGATGCAGATCTTGCCAACCTTC  
TTTTGGACGAGTACTTCTTGGATGTTACTGCTAAGTACCAACAAGCAGTACGTGATATCG  
TAGCTCTTGCGGTTCAAGCAGGTGTGCCAGTGCCAACTTTCTCAGCAGCTATTACTTACT  
TTGATAGCTACCGTTCAGCTGACCTTCCAGCTAACTTGATCCAAGCACACGTGACTACT  
TTGGTGCTCACACTTACCAACGTAAAGACAAAGAAGGAACCTTCCACTACTCTTGGTATG  
ACGAAAAATAAGTAGGTCAGCCATGGGGAAACGGATTTTATTACTTGAGAAAGAACGAAA  
TCTAGCTCATTTTTTAAGTTTGGAACCTCCAGAAAGAGCAGTATCGGGTTGATCTGGTAGA  
GGAGGGGCAAAAAGCCCTCTCCATGGCTCTTCAGACAGACTATGATTTGATTTTATTGAA  
TGTTAATCTGGGAGATATGATGGCTCAGGATTTTGCAGAAAAATTGAGCCGAACCTAAACC  
TGCCTCAGTCATCATGATTTTAGATCATTGGGAAGACTTGCAAGAAGAGCTGGAAGTTGT  
TCAGCGTTTTGCAGTTTCATACATCTATAAGCCAGTCCTTATCGAAAATCTGGTAGCGCG  
TATTTTCGGCGATCTTCCGAGGTCGGGACTTCATTGATCAACACTGCAGTCTGATGAAAGT  
TCCAAGGACCTACCGCAATCTTAGGATAGATGTTGAACATCACACGGTTTATCGTGGTGA  
AGAGATGATTGCTCTGACACGCCGTGAGTATGACCTTTTGGCGACACTTATGGGAAGCAA  
NGAAGTATTGACTCGTGAGCAATTGTTGGAAAGTGTTTGGAAAGTATGAAAGTGCGACCGA  
GACAAATATCGTAGATGTCTATATCCGCTATCTACGGAGCAAGCT

## ORF Predictions:

ORF #	Start	End	Direction	Length
8	1697	1843	R	49 aa

[SEQ ID NO: ] 3860296-8 ORF translation from 1697-1843,  
direction R

VMFNIYPKIAVGPWNFHTAVLINEVPTSEDRRNTRYQIFDKDWLIDV\*

## Blastp and/or MPSearch Result:

## Description:

unknown

Assembly ID: 3860406

Assembly Length: 1578bp

[SEQ ID NO: ] 3860406 Strep Assembly -- Assembly  
id#3860406

CTACACCGGTTTGGTTAAAAATCGTATGCAAACCAAGGAGGCTTGGAGTCAGATTGATGT  
TCAGTTGAAACGTCGAAATGACCTCTTGCCAACTTGATTGAGACTGTAAAAGGTTATGC  
CAAATATGAAGGTTCTACCTTGAAAAGGTGGCAGAACTACGTAACCAAGTGGCGGCAGCG  
AATTCACCAGCAGAAGCTATGAAAGCCAGTGATGCCCTCAATCGTCAGGTTTCAGGTATT  
TTTGCAGTTGCAGAAAGCTATCCAGATTTGAAAGCTAGTGCTAACTTTGTTAAATTGCAA  
GAGGAGTTGACAAATACAGAAAATAAAATTTCTTACTCTCGTCAACTCTATAACAGTGTT  
GTCAGCAACTACAATGTAAAATTAGAACTTTCCCGAGCAATATTATCGCTGGAATGTTT  
GGATTTAAAGCGGCAGATTTCTTCAAACACCTGAAGAGGAAAAGTCGGTTCCTAAAGTT  
GATTTTAGCGGTTTAGGTGACTAAGATGTTGTTTGATCAAATTGCAAGCAATAAACGAAA  
AACCTGGATTTTGTGCTGGTATTTTCTTACTCTTAGCTCTTGTTGGTTATGCGGTTGG  
TTATCTCTTTATAAGATCTGGACTTGGTGGTTTGGTTATCGCACTGATTATCGGCTTTAT  
CTACGCTTTGTCTATGATTTTCAATCGACAGAGATTGTCATGTCCATGAATGGAGCGCG  
TGAGGTGGATGAGCAAACGGCACCAGACCTCTACCATGTAGTGGAAGATATGGCTCTGGT  
CGCTCAGATTCCTATGCCCCGTATTTTCATCATTGATGATCCAGCCTTAAATGCCTTTGC  
GACAGGTTCTAATCCTCAAAATGCGGCTGTTGCTGCGACTTCAGGTCTACTAGCTATCAT

GAATCGTGAAGAACTAGAAAGCTGTTATGGGACATGAAGTCAGTCATATTCGTAATTATGA  
TATCCGTATTTTCGACTATTGCAGTTGCCCTTGCTAGTGCTATCACCATGCTTTCTAGTAT  
GGCAGGTCGTATGATGTGGTGGGGTGGAGCAGGTCGCAGACGAAGTGATGATGACCGAGA  
TGGAATGGTCTTGAAATCATTATGCTAGTGGTTTCCCTACTAGCTATTGTACTGGCACC  
TCTCGCTGCAACCTTGGTTCAGCTCGCTATTTCTCGTCAGAGGGAATTTCTGGCAGATGC  
ATCTAGTGTGCGAGCTGACTCGCAATCCCCAGGGAATGATTAATGCCCTAGATAAGTTGGA  
CAATAGCAAACCTATGAGTCGCCACGTCGATGATGCTAGCAGTGCCCTTTATATCAATGC  
TCCCAAGAAAGGTGGGGGGGTCCAAAACTCTTTTATACCCACCCACCTATCTCAGAACG  
GATTGAACGTTTAAACAGATGTAAAATGAAGGCTGGAAAAAAGTCTTTAAAATCTGAAA  
AATGCATAATATCAGGTGTGAAAACCTGATATTATGCGTTTTACTATGGGAAGATTTACT  
TCTTTTCTCCTAAATTTGTGTTTTTGCCCCACCTATCTGCTATGTTGCAAATTCGATAA  
ATCTTCTAAATTAAGTAG

## ORF Predictions:

ORF #	Start	End	Direction	Length
6	148	504	F	119 aa
7	497	1405	F	303 aa

[SEQ ID NO: ] 3860406-6 ORF translation from 148-504,  
direction F  
VAELRNQVAAANS PAEAMKASDALNRQVSGIFAVAESYPDLKASANFVKLQEELTNTENK  
ISYSRQLYNSVVSNNYVKLETFPSNIIAGMFGFKAADFLQTPEEEKSVPKVDFSGGLGD\*

## Blastp and/or MPSearch Result:

Description:  
unknown

[SEQ ID NO: ] 3860406-7 ORF translation from 497-1405,  
direction F  
VTKMLFDQIASNKRKTWILLLVFFLLLLALVGYAVGYLFIRSGLGGLVIALIIGFIYALSM  
IFQSTEIVMSMNGAREVDEQTAPDLYHVVEDMALVAQIPMPRIFIIDDPALNAFATG SNP  
QNAAVAATSGLLAIMNREELEAVMGHEVSHIRNYDIRISTIAVALASAITMLSSMAGRMM  
WWGGAGRRRSDDDRDNGLEIIMLVVSLLAIVLAPLAATLVQLAISRQREFLADASSVEL  
TRNPQGMINALDKLDNSKPMRHHVDDASSALYINAPKKGGGVQKLFYTHPPISERIERLK  
QM\*

Blastp and/or MPSearch Result:

Description:

HEAT SHOCK PROTEIN HTPX PRECURSOR. - ESCHERICHIA COLI.

Assembly ID: 3860416

Assembly Length: 1644bp

[SEQ ID NO: ] 3860416 Strep Assembly -- Assembly  
id#3860416

TTTTTACCACTTCACCGGAGTTTTTCTTCCTTAACTTCCATCAGGATTAATCGCTGTAAA  
GATACGTTTCTTTAACCAGTTTTTCCTTCTTGTCNACACGAGTTTCACCTAGAAACAGT  
GTTGAATCTTTTTTCTCAACTGTCTTGAAGGCCAAATCTTTTCAACAAAATTTTCGAGTT  
GTGGGGAAGATCTTCTTGTAACAGCAGCAACTGTCTTTCTCCAGAACTGGTTTTTCCC  
TTAGTCAACTGGATACCGGTATTCCTTAACTTGTTTTCCACTTTCTGAAACGAGGCGAAC  
AAGTACTGGAAGGCAATCTTCTCCACTATCTACCACAGTTGAAGCTACTTGATTGTTTTT  
TTCAACTGAGACTTTTGGCCGTTGACCTTTATAGGTAATTTGATAGTCTTGACGATTTTC  
AGCGAAATCAGCAAGTTCTTTTCCATCTACAAGAATCTTCGATTGCGTGCTTTCTTGAGG  
CAATTCACTTGGTGCAAGGAAGGTCATCTCAATCATCGCAACACCGCTCTTATCTGCTTT  
ACGCTCCATACGCCATCTCATAGCTTTGGCTTTGACAGCTTTAAATGTTACGTTGATTTT  
ATCACCAGCTGCGATGTCTTTATCCGCACGATAAGGCACAGCTTCCCAATTTTCTGGATT  
GTTGAATGGATGGTCTGCGTCGTAGGCTTGGTAGTTTGAATAGTAGGTTGGCACTTCAAA  
CTCTGGACCGACATAGCGTTCTAAAACGAGTTTAGTTGGTGTCATCCGTACCACTATCTGC  
AAAGAAGTGAAGTTTGGCTTGCGCAACAGTCCGTTCTACAATCTTACCATTTTCACGGAA  
GATCACACCCGCTGATACTTCTGGATTAGAAGATGGTGTTGGAGACCAGTTTGTCCAACG  
ACGATTTTCTGAATGATCTCCGTCATTGAGATAGTCAACGCGGTCATGAGAGTTTTTGT  
AATATCATTGGTTGCTGAAGCAAAGGCCTGGTTACTGTTTTTCATCATAGTTAGGGTTATC  
TGAAAGAGCTTCGCCTAGTTTGTCTGTCACTCGTACAGTGACCTCAGCAACAAGATCACT  
ACCAAGGACATGGCCTCGAACGGTAAATTGACCTGCTTTTGTGTCAGATTTTCTGCTGGAAC  
TTCTTCCCATTCAACTGACAAATCTTTTGTTCGTAGCCGTCTTTACCTGTGAAGTAAAC  
TGGAACCTTAGTCGGCAATTCAAGTGCTTGACCTACTTGTAGCAAGCGAGCTTGTTTAAC  
CGCAGCAACTGGTTTATGAGAAAGTAAGTTCTTATCCTTAGTGAAGTGCAGACGGTATTC  
TCCTAAGATGTCGCCATTTTCAGCTTTCGCGATGACACGAACTGGCTCACCTTCACGAAC  
GCTTGGAACGACGGTAGCGAGACCATTGTTGCTAACACTTGCGCTGTGACTGCCGGAACCTT  
TCCCATCTACAGACTCAAGGTAGTATCTGTCAGATCAGGTTGAAGTTTGCTAAGTCTTTA  
CCGTCAACTTGGAATCTTGTGTCCTTGCTTGGCTGCCGCAACTTGTTTTCGCAAAGATTT  
GTACCTCTGTGATAACGTTCCCTAATTTGTTGTCTGCTCTCACCATGGCGAATACGAACAG  
CATAGGTTTCAACTTTATCAAGAG

## ORF Predictions:

ORF #	Start	End	Direction	Length
6	72	281	R	70 aa

[SEQ ID NO: ] 3860416-6 ORF translation from 72-281,  
 direction R  
 VENKLRNTGIQLTKGKTSFWRKTVA AVTRKIFPTTRNFVEKDLAFKTVEKKDSTLFLGET  
 RXEQEGKTG\*

## Blastp and/or MPSearch Result:

Description:  
 unknown

Assembly ID: 3860712  
 Assembly Length: 1087bp

[SEQ ID NO: ] 3860712 Strep Assembly -- Assembly  
 id#3860712  
 ATCGAATTGCAAGTATGGCCATTGTCTTTCTATGTTAGTTTCTTTTAAAGACTGTAAATC  
 AAGGAATCCCTTACTATTTCATAGCGTAACGATTCTACAGGATCCATTTTACTAATCTTAC  
 GCGCCGGGAAGTAGGCTGAGACATAACCAAGTAATAGAGCGAAAAGTAGAGTTCCTAAAA  
 CAGATAAAAGATTTAATTCAAAAACCTTAGTGATGGATGGGTAAAAGTGACTTACAATCG  
 CATTCGCCAAACTTCCCACCCCTTGTGCAACCAAAAATGCCAGCAGCAAGGCGATGCCTA  
 CAATCCAGATAGCCTCGTAAATAAAAATTCCTTTGACATCACGATTCTGATAACCAACTG  
 CTTTCATGACACCTATTTTCCTTGGAACGTTGCATGATATTGATGTAAATAATGATACCAA  
 TCATAACCGCTGCTACCACAATAGCTTGTGATGAAAGCACAAATCAATAATCCCTGAATAA  
 CACGAATAAAGGTAATCACAATATCAAGAACTCTCTGTAAAGAAAGCACAGTATACTTCT  
 TATTTTTCTGTAATTCTTCTGTTACTACTTTTGTCTGTGATGGATCTTTGAGTTCCAAGA  
 TAAATAAGATACAGCTTTCGTAAATCCAGCCTCTTTCAAAATCGTTTCCATTTGATGAG  
 ACAGCATGAAACTGTTGCTGTCCTCCATGTCATCTTCATCATTGATTACACGTACAATCT  
 TCGTTTGAAATTGAGCAATCTTACTAGTTTCGGCAGCACTTCTACAATGCTGACTGAGA  
 CTGATTTGCCAATAAGATCATTAGCTGTCAAATTTTTTCCTGTCTGTTTCATTCCAATTTT

TTAGTAAACTGCTTGGAATCGTTAATCCCTGTTTCATTTGTATCAGTATAGAGGGATCCAG  
 CCAACACTTTGTCCGTCTCATTATTACTAACAGAGATACTTGTATCATCATAAAGACTCA  
 CTACTTGAGCATAAGAAGCATCGTTTGACTCAAATCCATTTCTTGCCCATCTTTTCTTG  
 CCATCTATAGTAATATTTGACATGTTTCATCCCAAAGGACTCTCCAAATATTTAATAGAT  
 CGAGCCT

## ORF Predictions:

ORF #	Start	End	Direction	Length
6	74	499	R	142 aa

[SEQ ID NO: ] 3860712-6 ORF translation from 74-499,  
 direction R  
 VITFIRVIQGLLIVLSSQAIVVAAMIGIIIIYINIMQRSKEIGVMKAVGYQNRDVKGIFI  
 YEAIWIVGIALLLAFLVAQGVGSLANAIVSHFYPSITKVFELNLLSVLGLTVFALLLGYV  
 SAYFPARKISKMDPVESLRYE\*

## Blastp and/or MPSearch Result:

Description:  
 unknown

Assembly ID: 3860728  
 Assembly Length: 1283bp

[SEQ ID NO: ] 3860728 Strep Assembly -- Assembly  
 id#3860728  
 ATCGAATTGAAAAATACAGCATGCCTTTTGTCCAATTGGTACTTGAAAAAGGAGAAGAAG  
 ACCGTATCTTTTCAGACTTGACTCAAATCAAGCAAGTTGTTGAAAAACAGGTCTGCCTT  
 CTTTTTTAAACAAGTGGCAGTAGACGAGTCGGATAAGGAAAAACGAATTGCTTTTTTC  
 CAAGATTCTGTGTCGCCTTTATTACAAAACCTTTATCCAGGTTCTGGCCTACAATCACAGA  
 GCAAATCTTTTTTATGATGTGCTTGTAGATTGCTTGAACCGACTTGAAAAAGAAACAAAT  
 CGATTTGAAGTGACGATTACGTCTGCTCATCCTCTAACTGATGAACAGAAGACTCGTTTG  
 CTCCTTTGATTGAGAAAAAATGTCTCTGAAAGTAAGGAGTGTAAGAACAACAAATCGAT  
 GAAAGTCTCATTGGTGGTTTTGTTCATTTTTGCCAATCACAGACAATTGATGTGAGTATT

AAACAACAACCTTAAAGTTGTTAAAGAAAATTTGAAATAGAAAGTGGTGTCTTTTGGCAA  
 TTAACGCACAAGAAATCAGCGCTTTAATTAAGCAACAAATTGAAAATTTCAAACCCAATT  
 TTGATGTGACTGAAACAGGTGTTGTAACCTATATCGGGGACGGTATCGCGCGTGCTCATG  
 GCCTTGAAAATGTCATGAGTGGAGAGTTATCGAATTTTGAAAACGGCTCTTATGGTATGG  
 CTCAAAACCTTGGAGTCAACAGACGTTGGTATTATCATCCTAGGTGACTTTACAGATATCC  
 GTGAAGGCGATACAATCCGCCGTACAGGGAAAATCATGGAAGTCCCTGTAGGTGAAAGTC  
 TGATTGGTCGTGTTGTGGATCCGCTTGGTCGTCCAGTTGACGGTCTTGGAGAAATCCACA  
 CTGATAAAACTCGTCCAGTAGAAGCACCAGCTCCTGGTGTTATGCAACGTAAGTCTGTTT  
 CAGAACCATTGCAAACCTGGTTTGAAAGCTATTGACGCCCTTGTACCGATTGGTCGTGGTC  
 AACGTGAGTTGATTATCGGTGACCGTCAGACAGGGGAAAACAACCATTTGCGATTGATACAA  
 TCTTGAACCAAAAAGATCAAGATATGATCTGTATCTACGTCGCGATTGGACAAAAAGAAT  
 CAACAGTTTCGTACGCAAGTAGAAACACTTCGTCAGTACGGTGCCTTGGACTACACAATCG  
 TTGTGACAGCCTCTGCTTCACAACCATCTCCATTGCTCTTCCTAGCTCCTTATGCTGGGG  
 TTGCTATGGCGGAAGAATTCGAT

## ORF Predictions:

ORF #	Start	End	Direction	Length
6	259	519	F	87 aa

[SEQ ID NO: ] 3860728-6 ORF translation from 259-519,  
 direction F  
 VLVDCLNRLEKETNRFEVTITSAHPLTDEQKTRLLPLIEKKMSLKVRSVKEQIDESLIGG  
 FVIFANHKTIDVSIKQQLKVVKENLK\*

## Blastp and/or MPSearch Result:

## Description:

ATP SYNTHASE DELTA CHAIN (EC 3.6.1.34). - ENTEROCOCCUS  
 FAECALIS (STREPTOCOCCUS FAECALIS).

Assembly ID: 3860794  
 Assembly Length: 1402bp

[SEQ ID NO: ] 3860794 Strep Assembly -- Assembly  
id#3860794

CTAATCAATCCAAAAGGAGCAACCAAATAACTGGTCCACCATTCCCAATGAGCATCTGCA  
AAAAGTTTTCAACCCATAGCTGGCAATGCAATATTAAGAATGTCTTTATTTTTCTTAAAC  
AATCTCTCCTTCCTGATGAAAAGAACTCAGTTGGTTTCCCAACCGAGTTTACTCCCTCT  
ATCTTAAAGTCCTAAATAAGCCTCAACCGCTACTTGCATGTCAGCAGCTGCCACTGTTGT  
CTTGTGACGAACAGGAGCTGTCTCAAGCCCATCAACTGCTGGTGGCACTGCAACGCCTGA  
GATTTTCATGTAATTGAGCCAAAGCTTCAAAGTCTGTTAAACCTGCTTTTCCAGTTACAGC  
TTCTACTGCAACTACTGGGAACCTGTAGGGACTAGCTGTTGAAGCAATCACTGTCTTAGT  
CGCATCATCAGTAACCGCTTGGTATTTTCTATAAACTGCTGAGGCAACCGCCGTATGTGG  
ATCCTCAATATAAGAATCTAACTCATAAACACGCTTGATTTCTGCCGCTGTTTCTTCCTC  
AGTCGCATATTCAGCTGCAAAGAGCTCCAGAATCTCTACATCAAATCAGTCAGTTCATA  
TTGTCCTTGTGTATTCAAGGTATTCATGAGTTCAGCCGTCTTAACCGCATCATTCCCCAA  
AAGATGGAAAATCAAACGCTCCAAGTTTGAAGATACCAAGATATCCATAGATGGGCTGGT  
TGTTACCTTAAACTCACGTTTCTTGTCGTAAACACGTGTCTTGAAGAAGTCTGTCAAAC  
ATTGTTATCATTTGAAGCACAGATCAATTTACCAACTGGGAGACCGATTTGTTTGGCATA  
AAAGGCAGCCAAGATATTTCCAAAAGTTTCCTGTTGGTACTGTGAAGTTAATCTTATCAC  
CAGCCACGATCTCACCAGTCTTGACCAACTGAGCCATAGGCCATAAACATTAATTAAACA  
ATCTGTGGCACCCAAACGACCGCATATTCATAGAGTTTTAGCAGATGAAAATTGCAACCT  
TGTTGGCCGCTAATCTTTCACGAAGAGCCACGTTCGTAAACATGTGCTTCACGTTGGTTT  
GCGCATCGTCAAAGTTACCATCTATAGCGATAACATGAGTATTGTCACCATTATGAGTGG  
TCATTTGCAACTCTTGTTACCTTGCTGACACCACCCTTTGGATAAAAGACGATAATCTCAG  
TACCAGGCACATCCGCAAACCCCGCCATAGCAGCTTTCCCCGTGTCACCAGATGTGCGCTG  
TCAAGATAACAATCTTGTTCTCCAAACCATGTTTTTTTAGCAGCAGTCGTCATAAAGTATG  
GCAAATAGACNAGGCCATATCCTTAAAGGCAATNGTTGAACCATGGAAAAGTTCCAAAT  
TGTATTGCCCATCTAATTCGAT

#### ORF Predictions:

ORF #	Start	End	Direction	Length
6	184	915	R	244 aa

[SEQ ID NO: ] 3860794-6 ORF translation from 184-915,  
direction R

VRSWLVIRLTSQYQQETFGNILAAFYAKQIGLPVGKLIASNDNNVLTDFFKTRVYDKKR  
EFKVTTSPSMDILVSSNLERLIFHLLGNDVKTAEMLMNTLNTQGQYELTDFDVEILELFA  
AEYATEEETA AEIKRVYELDSYIEDPHTAVASAVYRKYQAVTDDATKTVIASASPYPFP  
VVAVEAVTGKAGLTDFEALQLHEISGVAVPPAVDGLTAPVRHKTTVAAADMQVAVEAY  
LGL\*



## Blastp and/or MPSearch Result:

## Description:

Probable threonine synthase

Assembly ID: 3860830

Assembly Length: 989bp

[SEQ ID NO: ] 3860830 Strep Assembly -- Assembly  
id#3860830

CTCTTCGTCACATGGAAGAAGTTGGATTCAAATCCTTCAATCTTGGTCCAGAGCCAGAAT  
TCTTCCTATTTAAGTTGGATGAAAATGGGGACCCAACACTTGAAGTGAATGACAAGGGTG  
GCTAATTGGAATTTGGCACCTTACTGACCTTGC GGACAACACACGTCGTGAGATTGTGAA  
TGTCTTGACCAAAATGGGATTTGAAGTAGAAGCGAGTCACCACGAGGTTGCGGTTGGACA  
GCATGAGATTGACTTTAAGTACGATGAAGTTCTCCCGTGCTTGTGATAAGATTCAAATCT  
TTAAACTTGTTGTTAAACCATTGCTCGCAAACACGGACTTTACGCAACATTTATGGCGA  
AGCCAAAATTTGGTATTGCTGGATCAGGTATGCACTGTAATATGTCCTTGTTTGATGCAG  
AAGGAAATAACGCCTTCTTTGATCCAAATGATCCAAAAGGAATGCAGTTGTCAGAAACAG  
CTTACCATTTTCCTAGGCGGTTTGATCAAGCATGCTTACAAC TACTGCCATCATGAACC  
CAACAGTTAACTCATACAAACGTTTGGTTCCAGGTTATGAAGCGCCTGTTTACATTGCTT  
GGGCTGGTTCGTAACCGTTTCGCCACTTGTGCGATCAGCGTACCTGCTTCACGTGGTATGGG  
AACTCGTCTTGAGTTGCGTTCA GTGGATCCAATGGCGAACCCTTACGTTGCTATGGCTGT  
TCTTTTGGAAGTTGGTTTGTATGGTATTGAAAATAAAATCGAAGCACCAGCTCCTATCGA  
AGAAAATATCTACATCATGACAGCAGAAGAGCGCAAGGAAGCTGGTATTACAGACCTTCC  
ATCAACTCTTCACAACGCTTTGAAAGCTTTGACAGAAGATGAAGTGGTTAAAGCTGCTCT  
CGGAGATCACATCTACACTAGCTTCCTTGAAGCCAAACGAATCGAATGGGCAAGTTATGC  
AACCTTCGTTTCACAATGGGAAATTCGAT

## ORF Predictions:

ORF #	Start	End	Direction	Length
6	176	286	F	37 aa

[SEQ ID NO: ] 3860830-6 ORF translation from 176-286,  
direction F

VNVLTKMGFEVEASHHEVAVGQHEIDFKYDEVLPCL\*

Blastp and/or MPSearch Result:

Description:

Glutamine Synthetase SAGLNAR NCBI gi: 468507 NCBI gi: 47374 -  
Staphylococcus aureus.

Assembly ID: 3860984

Assembly Length: 817bp

[SEQ ID NO: ] 3860984 Strep Assembly -- Assembly  
id#3860984

ATCGAATTTATCCGTAAGACCATTCAGCACTTGGCAAGTAATGGGTGTGATTTGATTTCGT  
CTAGATGCCTTTGCTTATGCAGTGAACGAAATTGGATACTAATGATTTCTTTGTGGAACC  
AGATATTTGGGATTTATTGGACAAAGTTCGAGATATCGCTGCTGAGTATGGGACAGAGCT  
TTTACCTGAGATTCATGAACACTATTTCGATTCAGTTTAAAATAGCAGACCATGATTACTA  
TGTTTATGATTTTGTCTCTTCCAATGGTGACACTTTATACTCTTTACAGTTCCAGAACAGA  
GCGTTTGGCTAAGTGGTTAAAGATGAGCCCGATGAAGCAATTTACGACGCTAGATACCCA  
TGATGGGATTGGAGTAGTAGATGTCAAGGATATCCTGACCGATGAGGAGATTGACTATGC  
TTCAAATGAACTCTATAAGGTTGGAGCCAATGTCAAACGTAAGTACTCTAGTGCCGAGTA  
TAACAACTTAGATATCTTACCCAAAATCAATTCAACCTAACTTATTCAGCGCTTGGAGAT  
GATGATGTCAAGTATTTTCTCGCTCGTCTAATTCAAGCTTTTGCCCCAGGTATTCCTCAG  
GTTTACTATGTGGGTCTATTAGCAGGCAAGAATGACTTGAAATTATTAGAAGAACTAAA  
GAAGGTCGAAATATTAATCGTCATTACTATAGCAACGAGGAAATAGCAAAAGAAGTGCAA  
CGACCTGTTGTGAAGGCCCTTCTCAATCTATTTTCTTTCCGTAACCGTTCAGAAGCCTTT  
GATCTAGAAGGGACTACTGAGATAGAGACACCAACAG

ORF Predictions:

ORF #	Start	End	Direction	Length
6	113	520	F	136 aa

[SEQ ID NO: ] 3860984-6 ORF translation from 113-520,  
direction F

VEPDIWDLDDKVRDIAAEYGTPELLPEIHEHYSIQFKIADHDYVYDFALPMVTLYTLYSS  
 RTERLAKWLKMSPMKQFTTLDTHDGIGVVDVKDILTDEEIDYASNELYKVGANVKRKYSS  
 AEYNNLDILPKINST\*

Blastp and/or MPSearch Result:

Description:

sucrose phosphorylase (EC 2.4.1.7) - Streptococcus mutans

Assembly ID: 3861088  
 Assembly Length: 556bp

[SEQ ID NO: ] 3861088 Strep Assembly -- Assembly  
 id#3861088  
 ATCGAATTTGCTCTAATAACAAGTTTTTTGGTCAAAGACCCCGTCTTAGTGGAAGCATC  
 CCCATTCCAGATGGAGTTTTTTCACGATCACATAATCAACGTGTTTAAGGTCAGCAACCTG  
 ACGTCCACCTGCATAAGAAATAGCACTTTGAAGGTCTTGTTCCATCTCAGTTAAAGTGTC  
 TTGCAGATGACCTTTAGCAGGAAGCAAGATACGTTTGCTCCACATTTTTGTAAAGCACC  
 TTTTTGATATTGTGAGGCTGAACCATAATATCCTCTGAACTGTCCACCATCGACTTCAAT  
 CGTTTCCCCTGGACTTTCAATGTGTCCTGCAAAGAGGGAACCAATCATGATCATGCTAGC  
 ACCGAAGCGGATAGACTTAGCAATATCACCGTGAGTACGAATTCCTCCATCAGCGATAAT  
 CGGTTTACGCGCAGCCTTGGCACACCAGCGTAAGAGCAGCCAACTGCCAACCACCTGTTA  
 CCAAACAGTCTTAACCTTGGTGATACAAACCTTACCAGGACGGATTCCGACCTTAGTA  
 CCATCCGCACTAGCAT

ORF Predictions:

ORF #	Start	End	Direction	Length
6	46	474	R	143 aa

[SEQ ID NO: ] 3861088-6 ORF translation from 46-474,  
 direction R  
 VVGSWLLLRWCAKAARKPIIADGGIRTHGDIKASIRFGASMIMIGSLFAGHIESPGETIE  
 VDGGQFRGYYGSASQYQKGAYKNVGGKRILLPAKGHLQDTLTEMEDLQSAISYAGGRQV  
 ADLKHVDYVIVKNSIWNGDASH\*

Blastp and/or MPSearch Result:

Description:

inosine-5'-monophosphate dehydrogenase (guaB) homolog -  
Haemophilus influenzae (strain Rd KW20)

Assembly ID: 3861138

Assembly Length: 528bp

[SEQ ID NO: ] 3861138 Strep Assembly -- Assembly  
id#3861138

AAAAAGCCAGAGGAGTGTGAGGAAGTGGAAAATCGAAAATTGTGAAGGATATCTTATTTT  
TATCTCAAGTGTCTCAGCCGGCAAGTCAGGAGGACCTTTATCTTGCCAGAGATTTGCAGG  
ATACACTCTTAGCAAATCGTGATACCTGTGTTGGTCTAGCTGCCAATATGATTGGGGTGC  
AGAAGCGCGTGATTATCTTTAATCTTGGCTTAGTTCCTCGTGGTCATGTTTAACCCAGTGC  
TTCTGTCCTTTGAAGGATCTTATGAGGCAGAAGAAGGCTGTTTGTCTTGGTAGGTGTGA  
GATCAACTAAGCGTTATGAAACCATAAGGCTTGCCTATCGTGACAGCAAGTGGCAGGAAC  
AGACCATTAACCTTGACAGGCTTCCCAGCTCAGATTTGCCAGCATGAGCTGGATCACTTGG  
AAGGACGAATCATTTAGGAAGGAAAGCAAATGAAACGAATAGTCTTTGAACTTATTTTTA  
TCGCAACGACCTGGGTATATCTTTTTACCGCCCCCTTAACCTGACCAGC

ORF Predictions:

ORF #	Start	End	Direction	Length
6	42	437	F	132 aa

[SEQ ID NO: ] 3861138-6 ORF translation from 42-437,  
direction F

VKDILFLSQVSQPASQEDLYLARDLQDTLLANRDTCVGLAANMIGVQKRVIIIFNLGLVPV  
VMFNPVLLSFEGSYEAEEGCLSLVGVRSTKRYETIRLAYRDSKWQEQTITLTGFPAQICQ  
HELDHLEGRII\*

Blastp and/or MPSearch Result:

## Description:

fms protein homolog - *Thermus aquaticus* (fragment)

Assembly ID: 3861256

Assembly Length: 638bp

[SEQ ID NO: ] 3861256 Strep Assembly -- Assembly  
id#3861256

```
CTTAGGTCATTTTTTAAAATTCAAATTCGCAAGAACATCTTGCCCACTGGTGACCAATTT
TGCTCCTTCTTGAATCAAATGATGGCAACCGTCTGATAGTCCATCTAAAATGCTACCAGG
AATAGCAAAGATATCGCGTCCTTCTTCCATTGCTCGCTCACAGGTAATGAGACTACCTGA
ACGCATCTTAGCCTCTGCTACAATCACACCACGACAAAGTCCAGCAATGATGCGATTACG
GGCAGGAAAATCGAAATTTTCAGAGGTTGTTTCGCCAGATCCATATTTCACTTAGAGCCAGAT
GGTCATTGCCGATGTAGTCTTGCAAGCGTTTGTGGCTTTAGGATAAAACACATCCAGTC
CTGTTCCAATCACTGCAATGGTTTTTTCGCCATTCTGAAAAGCTGCCATATGAGCTGCTG
TGTC AATGCCCTTGGCCAGACCACTGACAATAACCAGTTCATTTTCCAAGCCTTGAATGA
CTTTTTCACTGACTTAGCTCCCTGTTTGCTACAAGCACGAATGCCCACGAACGCTACCT
TCCGGGAATTTCAAGGAAGGTCAAGATTTCCCTTGTTAAAATAAAAATACAGGCGCATC
ATATTATTTCACTCCAAATCCCCAAGGGATAACAAGTC
```

## ORF Predictions:

ORF #	Start	End	Direction	Length
6	13	207	R	65 aa
7	236	529	R	98 aa

[SEQ ID NO: ] 3861256-6 ORF translation from 13-207,  
direction R

VIVAEAKMRSGSLITCERAMEEGRDIFAIPGSILDGLSDGCHHLIQEGAKLVTSGQDVLA  
EFEF\*

Blastp and/or MPSearch Result:

Description:

SMF PROTEIN. - ESCHERICHIA COLI.

[SEQ ID NO: ] 3861256-7 ORF translation from 236-529,  
direction R  
VGIRACSKQGAKSVEKVIQGLENELVIVSGLAKGIDTAAHMAAFQNGGKTI AVIGTGLDV  
FY PKANKRLQDYIGNDHLALSEYGSGEQPLKFRFSCP\*

Blastp and/or MPSearch Result:

Description:

SMF PROTEIN (FRAGMENT). - BACILLUS SUBTILIS.

Assembly ID: 3861262

Assembly Length: 1727bp

[SEQ ID NO: ] 3861262 Strep Assembly -- Assembly  
id#3861262  
NCAAAAAATGTAGTGATTACGGGAGCAACTTCAGGAATCGGGAAGCGATTGCGCGTGCTT  
ATCTGGAGCAGGGTGAGGATGTCGTTCTAACAGGACGACGGATAGACAGATTAGAAATCC  
TTCAAGTCGGAGTTTGCAGTAAGCTTTCCAAATCAAACCGTCTGGACTTTTCCACTAGAT  
GTGACGGATATGGTCATGGTGAAGACTGTTTGCTCTGATATTCTAGAAACGATAGGGAGG  
ATTGATATCTTGGTCAACAACGCCGACTGGCTCTTGGCTTGGCTCCCTATCAAGACTAT  
GAGGAGTTGGATATGTTGACCATGTTGGATACCAATGTTAAAGGTCTGATGGCGGTTACT  
CGCTGTTTCTTGCCAGCAATGGTAAAAGTCAATCAAGGTCACGTTATCAATATGGGGTCA  
ACCGCAGGAATCTACGCCTATGCTGGTGCCGCTGTTTACTCAGCTACCAAGGCTGCGGTT  
AAGACCTTTTCGGATGGACTGCGAATTCGATACCATCGCAACGGATATCAAGGTGACAAC  
CATTCAGCCTGGGATTGTGAAACAGATTTCTCAACTGTTTCGTTTTTCATGGTGATAAAGA  
GCGGGCTGCGTCCGTTTACCAAGGAATAGAAGCCTTGCAAGCTCAGGATATTGCAGACAC  
AGTAGTCTATGTGACCAGTCAGCCTCGCCGTGTTTCAGATTACAGATATGACCATTATGGC  
CAATCAACAGGCGACAGGTTTCATGATTCATAAAAAATAAGAAATTTCCCTCGAAAAGTTA  
CAAATTTCTGTAACCTTTTTTTGATTTTCTTACGAATAGATAAGTAGGAGGAAGAAAATATGT  
ATAATAAAGTTATCATGATTGGGCGTTTAAACGTCTACACCAGAATTGCACAAAACCAACA  
ATGACAAGTCGGTAGCGCGAGCAACTATCGCTGTGAACCGTCGTTACAAAGACCAAAAACG  
GTGAACGTGAAGCTGATTTTGTTCATATGGTCCCTATGGGGCCAGAACTAGCCAGAAAA  
CTTTGGCAAGCTACGCAACCAAGGTAGTCTCATTTCCGTTGATGGAGAATTGCGTACCC  
GTCGCTTTGAGAAAAATGGCCAAATGAACTACGTGACCGAAGTACTTGTACAGGATTCC  
AACTCTTGGAAGTCGTGCTCAACGTGCCATGCGTGAAAATAATGCAGGCCAAGATTTGG

CAGATTTAGTCTTGGAGAAGAAGAATTGCCATTTTAATACTCTTCGAAAATCTCTTCAA  
 ACCACGTTAGCTTTATCCACAACATCAAAGCAATGCTTTGAGCAGCCTGCGGCTAGCTTC  
 CTAGTTTGCTTTTTTGATTTTTTATTGAGTGTTAGTTACTTGATAGCTTCGACCAAGTCTTG  
 AGCTTGTTTTTCAAGTGAGTTTAGGACTGTTTCTTCAAGAACCAATTTTCCGTCTGCCCCA  
 GGCAGAGTCATTAACACGTGCAGCAGTGAAATCACCAACGCCTTGTGTACGGATAAATGG  
 CAAGAGGTCTTTGTAGATAGCGAAAAGTTGATCGTGCCCTGCATTGGCTACAGATGATAC  
 TGTGACAACTTGTCTTGAAGGGCAGAAACGCCACGTGTATCAGACAAGTCAAGGGCAGC  
 AGATAGCCAGTCAAGCAAGTTTTTCACTGTACCAGGGATAGAGAAGTTGTAGACTGGAGA  
 GAAAATCCAGATAGCATCCGCAACGAGAACTGCTTCACGAGCAGCAG

## ORF Predictions:

ORF #	Start	End	Direction	Length
6	181	594	F	138 aa

[SEQ ID NO: ] 3861262-6 ORF translation from 181-594,  
 direction F  
 VTDMVMVKTVCSDILETIGRIDILVNNAGLALGLAPYQDYEELDMLTMLDTNVKGLMAVT  
 RCFLPAMVKVNQGHVINMGSTAGIYAYAGAAVYSATKAAVKTFSDGLRIRYHRNGYQGDN  
 HSAWDCRNRFLNCSFSW\*

## Blastp and/or MPSearch Result:

## Description:

HYPOTHETICAL OXIDOREDUCTASE IN DCP 3'REGION (FRAGMENT). -  
 ESCHERICHIA COLI. (BLAST)

Assembly ID: 3864150

Assembly Length: 3808bp

[SEQ ID NO: ] 3864150 Strep Assembly -- Assembly  
 id#3864150

AACTGGAACAAATATGGTTTTGTTCAAAACACCAATACCGTAAGGTTGACCGTGAAACAG  
 GTGTTGTACGAACGAAATTTGTTTGGTTGACAGCTGATGAAGAAGATGAATATACTGTAG  
 CTCAGGCTAACTCTCGTCTGAATGAAGATGGAACCTTTGCTGACAAGATTGTCATGGGAC

GTCACCAAGGGGTCAACCAAGAGTATCCAGCTAATATTGTTGACTACATGGACGTTTCAC  
CAAAACAGGTAGTTGCCGTTGCGACAGCATGTATTCCTTTCTTGAAAAACGATGACTCCA  
ACCGTGCCCTCATGGGAGCCAATATGCAACGTCAGGCTGTGCCATTGATTAATCCTCAGG  
CACCTTACGTTGGTACTGGTATGGAATACCAAGCAGCCCACGATTCTGGTGCGGCTGTGA  
TTGCTCAGTATGATGGTAAAGTTACTTACGCAGATGCTGACAAGGTAGAAGTTCGTCTGTG  
AAGATGGTTCATTGGATGTTTACCACATCCAAAAATTCCGTCGTTCAAACCTCAGGTACTG  
CTTACAACCAACGCCTCTCGTAAAAGTTGGTGATGTCGTTGAAAAAGGCGATTTTCATCG  
CTGACGGACCTTCTATGAAAAATGGAGAAATGGCGCTTGGACAAAACCCAATCGTTGCCT  
ACATGACTTGGGAAGGTTACAACCTTCGAGGATGCCGTTATCATGAGCGAACGCTTGGTGA  
AGGACGATGTCTACACATCTGTTTACCTTGAAGAATACGAATCAGAAACGCGCGATACAA  
AGCTTGGGCCTGAAGAAATCACTCGCGAAATTCCAAACGTTGGTGAAGATGCCCTCAAAG  
ACCTTGACGAAATGGGGATTATCCGTATTGGTGCTGAGGTTAAAGAAGGTGATATTCTTG  
TAGGTAAAGTAACACCTAAGGGTGAGAAAGATCTTTCAGCTGGAAGACGTCTCTTGAC  
GCTATCTTTGGAGACAAGTCTCGTGAAGTGCGTGATACTTCTCTTCGTGTACCACACGGT  
GCCGATGGTGTCTGTTTCGTGATGTTAAGATCTTTACACGTGTAAATGGAGATGAGTTGCAA  
TCAGGTGTTAACATGTTGGTTCGTGTTTACATCGCTCAAAAACGTAAGATTAAGGTCGGA  
GATAAAATGGCCGGACGTCACGGAAACAAAGGGGTGTCTCTCGTATCGTTCCTGTAGAA  
GACATGCCTTACCTTCCAGACGGAACCTCCAGTCGACATCATGTTGAACCCACTTGGGGTG  
CCATCACGTATGAATATCGGTCAGGTATGGAGCCTCACCTTGGTATGGCAGCTCGTACT  
CTTGGTATTCACATTGCGACACCAGTCTTTGATGGAGCAAGTCCTGAAGATCTTTGGTCA  
ACTGTTAAAGAAGCAGGTATGGATAGCGATGCCAAGACAATCCTTTACGATGGACGTACA  
GGTGAACCATTTGATAACCGTGTTTCTGTTGGAGTCATGTACATGATCAAACCTCCACCAC  
ATGGTTGACGATAAAATTGCACGCGCGTTTCAAGTCCGACCTTATTCAACTGTTACCCAAACA  
CCACTCGGAGGTAAAGCTCAGTTTGGTGGACAACGTTTTCGGTGAGATGGAGGTTTGGGCT  
CTTGAAGCCTACGGTGCGTCAAATGTCTTCAAGAAATCTTGACTTACAAGTCTGACGAT  
ATCAACGGACGTTTGAAGCCTATGAAGCTATTACAAAAGGCAAACCAATTCCAAAACCA  
GGTGTTCAGAAATCCTTCCGAGTTCTTGTCAAAGAATTGCAATCTCTTGGTCTTGACATG  
CGTGTCTTAGACGAAGATGACCAAGAAGTGGAACCTTCGCGACTTGGATGAAGGAATGGAC  
GAAGATGTCATCCACGTAGATGACCTTAAAAAGCCCGCGAAAAAGCAGCCCAAGAGGCT  
AAAGCAGCCTTTGAAGCTGAAGAAGCTGAGAAAGCAACAAAAGCGGAAGCAACAGAAGAA  
GCTGCTGAACAAGAATAAGCAGTTCACCTAGAATAGAAAGGGAAGAAATAGTGGTTGATG  
TAAATCGTTTTAAAGTATGCAAATCACCTTAGCTTCTCCAAGTAAAGTCCGTTTCATGGT  
CTTATGGAGAAGTCAAAAACCTGAAACAATCAATTACCGTACCTTGAACCCAGAACGTG  
AAGGACTCTTTGATGAAGTGATCTTTGGTCTTACAAAAGACTGGGAATGTGCTTGTGGTA  
AGTACAAAACGCATTTCGTTACAGAGGAATTGTTTGTGACCGCTGTGGGGTTGAAGTAACGC  
GTACGAAAGTTCGTGCGTGAGCGTATGGGACATATCGAATTGAAAGCTCCTGTATCTCACA  
TCTGGTACTTCAAGGGGATTCCAAGCCGTATGGGCTTGACCCCTTGATATGAGCCCTCGTG  
CCCTCGAGGAAGTTATCTACTTTGCGGCTTATGTGGTGATTGATCCTAAGGATACACCAC  
TTGAGCACAAAGTCTATCATGACAGAGCGCGAATACCGAGAGCGCTTGCGTGAATATGGTT  
ATGGTTCATTTGTTGCTAAGATGGGTGCGGAAGCCATCCAAGACCTTTTGAAGCAAGTAG  
ATCTTGAAAAAGAAATTGCTGAACTCAAAGAAGAATTGAAAACCTGCTACTGGACAAAAAC  
GTGTCAAAGCCATCCGTCGTTTGGATGTTTGGATGCCTTTTACAAGTCTGGAAACAAAC  
CTGAATGGATGATTCTTAACATCCTTCCGGTTATCCCACCAGATCTTCGTCCAATGTAGC



AGGAATTCGATGGTGGCCCGTTTTGCCTCATCTGACTTGAATGACCTTTACCGCCGTGTT  
 ATCAACCGTAACAACCGTTTTGGCTCGTTTGCTTGAGTTAAATGCACCAGGTATCATCGTT  
 CAAAATGAGAAGCGTATGCTTCAAGAAGCAGTTGACGCTTTGATTGACAATGGTCGTCGT  
 GGTCGTCCAATCACAGGACCAGGTAGCCGTCCATTGAAATCATTGAGCCACATGCTTAAA  
 GGTAAACAAGGACGCTTCCGTCAAACTTGCTCGGTAAACGTGTTGACTTCTCAGGACGT  
 TCCGTTATCGCCGTTGGTCCAACCTCTTAAGATGTACCAATGTGGTGTGCCACGTGAAATG  
 GCGATTGAACTCTTTAAACCATTTGTCATGCGTGAAATCGTTGCCCGTGATATCGTGCAA  
 AACGTCAAAGCAGCTAAACGCTTGGTGGAACGCGGAGATGAGCGTATCTGGGATATCCTT  
 GAAGAAGTGATTAAAGAACACCCAGTGCTTTTGAACCGCGCACCGACCCCTTCACCGTTTG  
 GGTATCCAAGCCTTCGAGCCAGTCTTGATTGATGGTAAGGCTCTTCGCTTGCACCCACTT  
 GTCTGTGAAGCCTACAATGCTGACTTTGACGGGGACCAAATGGCCATCCACGTACCACTT  
 TCAGAAGAAGCACAAGCAGAAGCTCGTATCCTCATGCTAGCTGCTGAGCACATCTTGAAC  
 CCGAAAGATGGGAAACCGGTAGTTACTCCATCTCAGGACATGGTTTTGGGTAACACTACTAC  
 TTGACCATGGAAGAAGCTGGTCGCGAAGGTGAAGGAATGGTCTTCAAAGACCGTGACAAA  
 GCGGTTATGGCTTACCGCAATGGTTATGTTACCTCCACTCACGTGTTGGTATCGCAACA  
 GACAGCCTCAACAAGCCTTGGACAGAAGAGCAAAGACATAAGGTCTTGCTTACAACAGTT  
 GGTAATAATTCTCTTCAACGATATCATGCCAGAGGGGCTACCATACTTGCAAGAACCAAAC  
 AATGCCAACTTGACAGAAGCTGTTCCAG

## ORF Predictions:

ORF #	Start	End	Direction	Length
7	922	1998	F	359 aa
8	2031	2759	F	243 aa

[SEQ ID NO: ] 3864150-7 ORF translation from 922-1998,  
 direction F

VRKIFQLEERLLHAIFGDKSREVRDTSLRVPHGADGVVRDVKIFTRVNGDELQSGVNMLV  
 RVYIAQKRKIKVGDKMAGRHNKGVSRIVPVEDMPYLPDGPVDIMLNPLGVPSRMNIG  
 QVMEPHLGMAARTLGIHIATPVFDGASPEDLWSTVKEAGMDSDAKTILYDGRGTGEFPDNR  
 VSVGVMYMIKLHHMVDDKLHARSVGPYSTVTQQPLGGKAQFGGQRFGEMEVWALEAYGAS  
 NVLQEILTYKSDDINGRLKAYEAITKGKPIPKGPVPEFRVLVKELQSLGLDMRVLDEDD  
 QEVELRDLDEGMDEDVIHVDDLEKAREKAAQEAKAAFEAEAEKATKAEATEEAAEQE\*

## Blastp and/or MPSearch Result:

## Description:

DNA-DIRECTED RNA POLYMERASE BETA CHAIN (EC 2.7.7.6)  
 (TRANSCRIPTASE BETA CHAIN). - BACILLUS SUBTILIS.

[SEQ ID NO: ] 3864150-8 ORF translation from 2031-2759,  
direction F  
VVDVNRFKSMQITLASPSKVRWSYGEVKKPETINYRTLKPEREGLFDEVIFGPTKDWEC  
ACGKYKRIRYRGIVCDRCGVEVTRTKVRRERMGHIELKAPVSHIWYFKGIPSRMGLTLDL  
SPRALEEVIYFAAYVVIDPKDTPLEHKSIMTEREYRERLRREYGYGSFVAKMGAEAIQDLL  
KQVDLEKEIAELKEELKTATGQKRVKAIRRLDVLDAFYKSGNKPEWMILNILPVIPDLR  
PM\*

Blastp and/or MPSearch Result:

Description:

DNA-DIRECTED RNA POLYMERASE BETA' CHAIN (EC 2.7.7.6)  
(TRANSCRIPTASE BETA' CHAIN ) (FRAGMENT). - BACILLUS  
SUBTILIS.

Assembly ID: 3864190

Assembly Length: 2753bp

[SEQ ID NO: ] 3864190 Strep Assembly -- Assembly  
id#3864190

ACCCGCTTTCAGAACTTAAACAGATTGCGGATGTATTTGTAAATGGCAATCTATCTCTAG  
AAGTTCAGTGTAGTCCCTTGCCCTCAGAAAGTCCTTAAAGAGCGAAGTGAGGGCTATCGTA  
GTCAGGGTTACCAAGTACTGTGGTTGCTGGGTCAAAAACCTGTGGCTCAAGGAGCGTTTGA  
CTCGTCTACAGCAAGGTTTTCTTTATTTTCAGTCAAAACATGGGCTTTTATGTTTGGGAAT  
TAGACAAGGAAAAACAAGTTTTAAGACTCAAATACCTGATTTACCAGGATCTCCGCGGTA  
AACTCCATTATCAAATCAAGGAATTTTCCTATGGTCAAGGTAGTTTATTGGAATATTGC  
GTCTTCCCTATAAGAGACAAAAATATCTCATTTTACAGTTTCTGAGGACAAGGACATCT  
GTCGCTATATCCGGCAACAACCTTTATTATCAAAATCTCTTTTGGATGAAAGAACAAGCAG  
AAGCCTATCAAAGGGAGAAAAATATCCTGACTTATGGACTGAAAGAATGGTATCCACAAA  
TTCGACCAATAGTGGGCAAATTTTCCAGATTGAACAAGACTTGACTAGCTATTATCAGC  
ACTTTTATACCTATTACCAAAAAAATCCTCAAAATGATTGGCAAAAGCTTTATCCACCAG  
CCTTTTATCAGCAATATTTCTTGAAAAATATGGTAGAATAGAAAGGATGGAGGAATCTAA  
TGGTATTACAAAGAAATGAAATAAATGAAAAAGATACATGGGATCTATCAACGATCTACC  
CAACTGACCAGGCTTGGGAAGAAGCCTTAAAAGATTTAACAGAACAAATTGGAGACAGTAG  
CCCAGTATGAAGGCCATCTCTTGGATAGTGC GGATAACCTACTAGAAATCACTGAATTTT  
CTCTTGAAATGGAACGCCAGATGGAGAAGCTTTACGTTTATGCTCATATGAAGAATGACC

AGGATACACGTGAAGCTAAGTATCAAGAGTACTATGCCAAGGCCATGACACTCTACAGCC  
 AGTTAGACCAAGCCTTTTCATTCTATGATCCTGAATTTATGGAGATTAGCGAAAAGCAGT  
 ATGCTGACTTTTTAGAAAGCTCAACCAAAGCTGCAGGTTTATCAACACTATTTTGACAAGC  
 TCTTGCAAGGCAAGGATCACGTTCTTTCACAACGTGAAGAAGAATTCGATTGGCTGGAGC  
 TGGAGAAATCTTTGGTTCAGCAAGTGAAACCTTCGCTATCTTGGACAATGCGGATATTGT  
 GTTCCCTTATGTCCTAGACGATGATGGTAAAGAAGTTCAGCTATCTCATGGGACTTACAC  
 ACGTTTGATGGAGTCTAAAAACGTGAGGTTTCGCCGTGGTGCCTATCAAGCTCTTTATGC  
 GACTTACGAACAATTCACACACCTATGCCAAAACCTTGCAAACCAATGTTAAGGTGCA  
 AAATTCGATGCTAAAGTTCGTAACACAGAGTGCTCGTCATGCAGCTCTCGCAGCGAAT  
 TTTGTTCCAGAAAGTGTTTATGACAATTTGGTAGCAGCAGTTCGCAAGCATTGCGCACTC  
 TTACATCGCTATCTTGAGCTTCGTTCAAAAATCTTGGGGATTTTCAAGATGTAC  
 GATGTCTACACACCGCTTTCATCTGTTGAATACAATTTTACCTACCAAGAAGCCTTGAAA  
 AAAGCAGAAGATGCTTTGGCAGTCTTGGGTGAGGATTACTTGAGCCGTGTCAAACGTGCC  
 TTCAGCGAGCGTTGGATTGATGTTTACGAAAATCAAGGCAAGCGTTCAGGTGCCTACTCT  
 GGTGGTTCTTACGATACCAATGCCTTTATGCTTCTCAACTGGCAGGACAATCTGGACAAT  
 CTCTTTACTCTTGTTCATGAAACAGGTCACAGTATGCATTCAAGCTATACTCGTGAAACT  
 CAGCCTTATGTTTACGGAGATTACTCTATCTTTTTTGGCTGAGATTGCCTCAACTACCAAT  
 GAAAATATCTTGACGGAGAAATTATTGGAAGAAGTGGAAGACGACGCAACACGCTTTGCT  
 ATTCTCAATAACTTCCTAGATGGTTTCCGTGGAACAGTTTTCCGCCAAACTCAATTTGCT  
 GAGTTTGAACACGCCATTACCAAGCAGATCAAAATGGGGAGGTCTTGACAAGCGATTTTC  
 CTAATAAACTCTACGCAGACTTGAACCAAGAGTATTATGGTTTGAGTAAGGAAGACAAT  
 CCTGAAATCCAATACGAGTGGGCTCGCATTCACACTTCTACTATACTACTATGTATAT  
 CAATATTCAACTGGCTTTGCGGCCCGCTCAGCCTTGGCTGAAAAAATTGTCCATGGTAGT  
 CAAGAAGACCGTGACCGCTATATCGACTACCTCAAGGCAGGTAAGTCGGACTATCCACTT  
 AATGTCATGAGAAAAGCTGGTGTTGATATGGAGAAGGAAGACTACCTCAACGATGCCTTT  
 GCAGTCTTTGAACGCCGTTTAAATGAGTTTGAAGCCCTTGTTGAAAAATTAGGATTGGCA  
 TAAAATGGTTGAATCGTATAGTAAGAATGCTAACCATAACATGCGTCGTCCTGTCTGTCAA  
 AGAAGAAATGTAGACTTGATGCGTCAGCGTCAAAAGCAGGTACAGGTTTCTTGAAAGA  
 ATTGGAAGACTTTGCCCCGAAGGAAAATATTCCTATTATTCCCATGAAACGGTTGCTTA  
 TTTCCGTTTCTTATGGAACCATGCAGCCTAAAAATATTCTGGAAATTCGAT

## ORF Predictions:

ORF #	Start	End	Direction	Length
8	1259	1534	F	92 aa

[SEQ ID NO: ] 3864190-8 ORF translation from 1259-1534,  
 direction F

VFPYVLDDDGKEVQLSHGTYTRLMESKKREVRRGAYQALYATYEQFQHTYAKTLQTNVKV  
 QNSMLKFVTTTRVLVMQLSQRILFQKVFMTIW\*

Blastp and/or MPSearch Result:

Description:

ligoendopeptidase F - *Lactococcus lactis*

Assembly ID: 3864204

Assembly Length: 2140bp

[SEQ ID NO: ] 3864204 Strep Assembly -- Assembly  
id#3864204

CCAGTTTGGTTCTGCATGTTGTTGTAGGCAGGACGAGCGAGACGTTGGAAGTCTTCTTG  
ATAAGCCAAGAGGCCCCAGATACGGTCTTCTTATCCACTTCAAGACGGATGTAGAGTTG  
GTCGCCCTTCTTAGGCCAGAGTTCCTTGAGCACAGGGAGAATATCGAGTGACAACAACGA  
TTTCCTTGTGAGGAAGGCCTGTATCCACAAAGACACCCAAGTCCTTACGAACCTCTGTGA  
CACGTCCCCAACCAAATTGGTCCTGAGTGGCAGTCACTTCTAAGGTTGTCAGGCGGAGTT  
TTTGCTTCATATCCGTGTATGCAAAACCTTTGACCGTATCCCCTACTGTATGTTGGCCCT  
CTTCCTTAGCAAGAGCATAGGTTTGACCATCCTTTTGCACAAAGTAAAAACGGTCATTTT  
CATCGATGATCAGTCCAACGATAAACTTGCAAGATTTGTATTCATATTTCTTCTTTCG  
AATAAACTCAGCCAGCAATGCCAACTGAGTTTTTCTGTTTATTTTTAGACTTCCAAAAG  
TTCTTTCTCTTTGTTAGCAGTCATGTCGTCGATGTGTTTAAACAGCATCGTCTGTACTTT  
TTGAATATCTTTTTCAAGAGTCTTCAATTCGTCTTCAGTGATTTCTTTTGCTTTTCTTG  
TTTCTTAGCTTCGTCCATAGCATCGCGACGGATATTGCGGACAGCCACTTTAGCATTTTC  
GCCGACCTTCTTCACTTCTTTAGCAAGGTCACGACGAGTTTCTTCTGTAAGAGCTGGGAT  
AACCAAGCGAATCACAGAACCGTCATTAGCCGGTGTGATACCAAGATCAGAAGCGTTCAA  
GGCACGTTGATGTCTTTCAATGAAGACTTGTCAAATGGTGTACCAACAAAACACGCGC  
TTCTGGAATCGTAATTGAAGCGATTTGGTTAAGAGGAGTTTCGACTCCATAGTATTCTAC  
ATGTACACGGTCAAGCAAGCTTGCAATTGGCAGCACCAGCACGGATACCACCAAATTCACG  
AGCAAGTGATTGGTGAGACTGGGTCAATTCTCTCTTTAGCTTTTTCAATAATTACGTTAGC  
CATATTCTTTCTTATTCTTTCTTTCGATATTATTTGAAACTGTTGTTCCGATATTTTCA  
CCAAATACGACACGTTTGATGTTGCCTGATTGGTTCATGTTGAAGACAACCAAGTCAATG  
TCGTTGTCCATTGAGAGGGTTGAGGCTGTTGAGTCCATGATACGAAGACCTTTGTTGATA  
ACATCACGGTGGGTCAATTCTTCAAACCTTAACGGCTGTCTTGTCTTCTTAGGATCGGCA  
TTGTACACACCATCGACGCCATTTTTAGCCATGAGGATGGCATCTGCTTCGATTTTCAGCT  
GCACGAAGGGCCGCTGTTGTATCTGTGCGAGAAGTATGGTGAACCAATTCCAGCACCAAAG  
ATAACGATACGGCCTTTTTCAAGGTGACGAAGGGCACGTCCACGGACATAAGGCTCTGCC  
ACTTGTTCATAGCAATAGCTGTTTGTACACGCGTATCAACCCCACTTGTGTGCAATGAA  
TCTGCCATCACAAAGAGCATTCATAACAGTCCCAAGCATTCAGTGTAATCTGCCTGAACA

CGGTCCATACCTGCTTCTGCTGCAGGTTCTCCACGCCAGAGATTTCCCTCCACCAATAACA  
 AGGGCAATTTTCGATACCTAAGCTATGAACCTTCTTGAATCTCTTTTGCGATTGTTTGAACCT  
 GTTTGGATATCAATCCCTACGCCACGTTACCGGCAAGGGCTTCACCTGATAACTTGATT  
 AAAATACGTTTATACTTGGGATTCGCCATTTTCACTCTCCTTCTTTTCATCCTACCTATTT  
 TATCACAATTTCTAAGATTTTATAGTATCATGAACAATTCTTTCAAAAAAATTAGACAG  
 TCAAAAATTCCTCTAAGTCGGCAAGGGCACGCTCTGCAATTTTTTCATAACGAGCCTTCT  
 TATCACGGATACGCTCGCCTTCCAACCTCCTTGATGATCCCAAATTGACATTCATTGGTT  
 GGAAATGTTTGCTGTCGGCATGGGTAATGTAATGAGCTAAGCTTCCAATCGCTGTCGTCT  
 CGGGGAAAATAACCTCGCTTTCTTCTTGAAGAGACGAG

## ORF Predictions:

ORF #	Start	End	Direction	Length
8	1092	1835	R	248 aa

[SEQ ID NO: ] 3864204-8 ORF translation from 1092-1835,  
 direction R

VKMANPKYKRILIKLSGEALAGERGVGIDIQTVQTIKEIQEVHSLGIEIALVIGGGNLW  
 RGEPAAEAGMDRVQADYTGMLGTVMNALVMADSLQQVGVDTRVQTAIAMQQVAEPYVRGR  
 ALRHLEKGRIVIFGAGIGSPYFSTDTTAALRAAEIEADAILMAKNGVDGVYNADPKKDKT  
 AVKFEELTHRDVINKGLRIMDSTASTLSMDNDIDL VVFNMNQSGNIKR VVFGENIGTTVS  
 NNIEEKE\*

## Blastp and/or MPSearch Result:

## Description:

URIDYLATE KINASE (EC 2.7.4.-) (UK) (URIDINE MONOPHOSPHATE  
 KINASE) (UMP KINASE) (SMBA PROTEIN). - ESCHERICHIA COLI.

Assembly ID: 3864212

Assembly Length: 2545bp

[SEQ ID NO: ] 3864212 Strep Assembly -- Assembly  
 id#3864212

CTCGCAGTTCTTCCATAGCTAATTGCGCCAAACGTCCTGCCAAGGTTGAGTCTTGTCCCC

CAGAAATCCCTAGAACAAAGGTTTTTAGGAAGGGATGTTTTTTCAGATATCTTTTAAAGG  
AAAATCAAATAGAACGACGGATTTCTTCCGGTGGGGCATCAATCACTGGGTTTGACAACC  
CAGCTCTTGATAATCGGTTTCTGGCAAACTCATTCGTCTTCTCCCTTTCACCAAGGGCT  
TCCTTGCGCATCTTATCAATCAAAGTCCATCTTATCTTGCCATACGTCACGCGCCAAATC  
CACTGGATAGTGCTGCGGATTGAGCACACGCTTAAACTCATCCCACAACCTTGTCAAATTC  
CTTACGGGCATAATCCTGAATGTCAGTCAAAC TAGGCAAGTTGTAAACTAATATTCCTTC  
TTTGAAGATATCCACCAAGAGAGGAACGGCATCAAAATTACGAACCGTCTTCTTGATGTA  
TGTATAGGTCGGATGGAACATCTTGATTTCTGTCATGTCGCTAATATCCACACCATCATA  
AGTGATGTAGTCACCTTCTGACTTGCCTTTTTCACGACTGGTAATGCGCCACACCTGCTT  
CTTACCTGGCGTCGACACTTTTTCCGCATTATTAGACAGCTTAATCGTATTGCGCATCTG  
GCCGTTTTTCATCTTCGATTGCAACAATCTTGTAACCGCCCCAAGAGCGGGCTGGTCATA  
GGCTGTAATCAGCTTGGTACCCACACCC CAGACATCAATCTTGGCCTTTTGCATCTTGAG  
GTTAAGGATGGTATTTTCATCTAGATCATTAGAAGCATAAATCTTAGCCTCTGGAAATCC  
AGCCTCGTCCAGTTGCTGACGGACTTTCTTAGAAATGTAGGCAATATCCCCAGAGTCAAT  
CCGCACACCCATAAAGTTAATCTGATCACCCAGCTCACGCGCCACCTGAATGGCAGCTGG  
TACACCGATGCGAAGGGTATCATAGGTATCCACAAGAAAGACACAATTTCGATTTGTGGGT  
CGCAGCGTAAGCCTTGAAAGCCTCATAGTCATTGCCATAAACCTGTACCAAGGCATGGGC  
ATGGGTTCCTCAAAACAGGAATGTCAAAGAGCTTACCCGCACGCACGTTGCTGGTTCCATT  
GGCGCCACCAATCACCGCTGCGCGTGTTCCAGATGGCCGCATCCATTTCTTGAGCCCCGA  
CGTGTTCCAAACTCCATCAAGGGTTCATCTTCGATAACCAAACGAATACGAGTGCTTTGT  
CGCCACCAAGGTCTGGTAGTTGACGATGTTCAAAAGAGCCGTTTCGACCAACTGACATTG  
GGGTAGAGGTCCTTCCACCTGCACAATCGGTTTATTAGCAAAAACCAAATCCCCTTCTTG  
GGCAGAACGAACGGTCAACTCCAACCTTGAAATTGCGAAGGTAATCCAAGAACGCCCCATG  
ATAACCAAGCGACTCCAAATAGGCTATATCACTATCTGAAAAACGCAAGTCTTCAAGATA  
GTTTACAATTCTTTCCAAACCTGCAAAAACCGCATAGCCGTTCTTAAAGGCTGTTGGCG  
GAAATACACCTCAAAGACCGCCTTCTTATTGTAAATCCCTTGATCAAAGTAAACCTGCAT  
CATGTTGATCTGGTACAAGTCCGTGTGCAATGTCAAAC TATCATCTGGATACATACTTTT  
CCTACTTCCTTAGCTAGAAACCCATGAAAATTTTCAAGAACTTTCATGTATTCCAATAAA  
TTAGTACTATTATATCACATTTT TAGCTGGATTGAGAAAAGAGTAACAAGCTATTCTCCAC  
TCTCCAATTCATCCATATCTTGTTCAAATTTTTTCTGAGCCCATTTCGCCATAGCTCTTAA  
GACCAAGATTGCCAATAAAGACCCACGGAAGGTAAATGACATAAGTAATGACCCAAGCAG  
ACAGGTATTTAAAATTCAAAGGATTGTGCTGATAAATTTCTATGTTGAATTGATAATTCT  
GCAACATCAAAAGAGCCGTAATAGCCAAGGTTAGGAAAAACAACCCAAAATCGTAAAAT  
GAAAACGACTATAGTAGGTCAC TCCAGATAACGGGCACGATTGAAAAAGTAAAATGTCC  
CTATGATGATAACGATTAGCAGCATATTAGAATTAAAAAGGCTTGGTGCTAATACTGAAA  
TGATATAAGATAGGAGCGACAAAGCAATGCAGATATAGAACTTTCAGAGCCCGCTTTAT  
TGAACAGTTGTTCTTCTCTTTCGTCTAGTAATTGATAATAATAAAATCTATTTTTTCATCT  
TCTTCTCCCAAAATAGTTGGTCTAGGGTTTTCCCTAAACATCTGCAATAGACTGGCAG  
AGCGAGAGACTGGGATTGTATTTTCCCGCCTCTATCAAACCAATAGTCTGGCGTGTACC  
CCGACAGCCTCTGCCAGTTGACCTTGTGTTAAATCACGCTCTACCCGAGCTAATTTTAAT  
TTTAAATTTTTTAGCCACCTTCGTCTCCTTATAGTTTTTAATACTCATCTACGCTTAAAA  
ATCCAAAACCAACACAAGCTATCAG

## ORF Predictions:

ORF #	Start	End	Direction	Length
6	256	1155	R	300 aa

[SEQ ID NO: ] 3864212-6 ORF translation from 256-1155,  
direction R  
VIGGANGTSNVRAGKLFDPVVLGTHAHALVQVYGNDYEAFAKAYAATHKSNCVFLVDITYDT  
LRIGVPAAIQVARELGDQINFMGVRIDSGDIAYISKVVRQQLDEAGFPEAKIYASNDLDE  
NTILNLKMQKAKIDVWGVGTLITAYDQPALGAVYKIVAIEDENGQMRNTIKLSNNAEKV  
STPGKKQVWRITSREKKGKSEGDIYTYDGVDISDMTEIKMFHPTYTYIKKTVRNFDVPLL  
VDIFKEGILVYNLPSLTDIQDYARKEFDKLWDEFKRVLNPQHYPVDLARDVWQDKMDFD\*

## Blastp and/or MPSearch Result:

## Description:

unknown

Assembly ID: 3864214

Assembly Length: 3655bp

[SEQ ID NO: ] 3864214 Strep Assembly -- Assembly  
id#3864214

ACTTGATTAACAAATTTAACCTGCTAACTGCATCCAACGAATTCTTGGATCTTTAGCTTG  
GTTGCTTCCTCCCTGCCATGGCCATGTCTGGTTTACCACCACCACGTCCATCGATGATTA  
GTGCTAATTCTTTGACAAGGTTTCCTGCATGAAGGTCTTTTGCTTGCTTGCTACAAGGA  
CATTGACTTTGTCAACCGATAGCGGCAACTAGGACAAGAAGATCAGAGTAGTCTTTTTGTT  
TCCAGTTATCTGCAAAAGTACGAAGGGCACCGGCATCGGATACAGACACTTGACTAGCAA  
TGTAACGATGACCGTTGACTTCCTTAACATCTTTGAAGATATCGCCTGCGGCTGCAGCTG  
CGGCTTTTTCTTTCAACTCAGCATTTTCTTTTGAAGTTGACGAAGTTGTTCTTGAAGTC  
CTTCTACCTTGTGAGGTACTTCCTTGACTTGAGGTGCTTTCAAGGTTGCTGCGACAGCTT  
TAAGAGCATCTCTTGTTCACGATAGGCTTCAAAGGCTTCCTTACCAGTCACTGCCAAGA  
TACGGCGAGTTCCTGAACCGATTCTTCTTTGACAATTTTGAAGAGACCAATCTCAG  
AAGTGTTGCCAACATGAGTACCACCACAAAGTTCAATAGANTANTCACCGATAGTCACGA  
CACGAACCTNCCTTGNCGTATTTCTCACCNAGAGGGCNATANCTCCCATTTCTTTAGCAG

TGTCAATATCCGTTTCAACTGTCTTAACTTCAAGANCTTCCCAGATTTTTTCGTTGACTT  
GCTGTTCAATCGCACGCAATTCTTCAGCAGTTACAGCTTGGAAGTGGGTAAAGTCAAAGC  
GAAGGAATTCAACTTCGTTAAGAGATCCTGCCTGTGTTGCGTGGTTTCCAAGGATATTGT  
GAAGGGCAGCGTGAAGCAAATGAGTCGCAGTGTGGTTTTTTCATGACACGGTGACGGCGAT  
TGCTATCAATTGCCAAGGTATATTCTTGGTTCAAGGCAAGCGGTGCAAGGACTTCAACTG  
TATGAAGGGCTTGACCATTTGGGGCTTTCTGAACATTGGTTCACAGTAGCCACAACCTTAC  
CTGACTCATCCAAGATTTGTCCGTAGTCAGCTACCTGTCCACCCATTTTCAAGCATAAAATG  
ACGTTTTCCGCAAAGATAAGAGAGGCAGTTCCTTCTGAAACAGCTTCTACTTCTGCATTGT  
CCGCCACGATAGCTACCAATTTAGAAGACAATTGGCTAGCATTTGTAGTTGAAGGCACTTT  
CTACAGTGATGTTTTGAAGAGTTTCATTTTGCATACCCATTGAGCCACCCCTTGACAGCTG  
ACGCACGCGCGCGTTCTTGTGTTCTTTCATGGCTGCTTCAAACCTTCACGGTCTACAG  
TCATACCAGCTTCTTCAGCGATTTCTTCAATCGAATTCAACTGGGAACCCATAAGTATCA  
TAGAGTTTGAAGACATCTGAACCAGCGATAACAGATTGACCTTTTTCTTTCAAGTCTGCT  
ACAATGCCTTGGGCAAAGTGTTGACCTGAGTGAAGGGTACGGGCAAATGATTCTTCTTCG  
CTCTTAACGATTTTCTCAATAAAGTCACGTTTCTCAAGCACTTCTGGGTAGTAGCTTTCC  
ATGATTTTTTCCAACAGTTGGAACGAGTTTGTAAAGGAAAGGCTCGTTGATACCCAATTTT  
TGACCATGCATAGAAGCACGACGAGAGAAGACGACGAAGGACATAACCACGACCCTCATTT  
CCTGGAAGGGCACCATCACCGATGGCAAATGAAAGTGAACGGATGTGGTCAGCGATGACC  
TTGAAGCTCATGTTGTGCGCATCTTGGTCATAAACCTTACCAGACAATTTCTCGACTTCA  
CGGATAATCGGCATGAAGAGGTCCGTTTCAAAGTTGGTCTTAGCCCCCTTGATAACGGCC  
ACCAAACGCTCCAAACCAGCGCCCGTATCAATGTTCTTATGTGGCAATTCCTTGTATTCTG  
CTACGAGGAACAGCAGGGTCTGCGTTAAATTGTGACAAAACGATGTTCCAGATTTCAATA  
TAACGGTTCGTTTTCAATATCTTCTGCAAGCAGGCGAAGACCGATATTTTCTGGGTCAAAG  
GCTTCCCCACGGTCAAAGAAGATTTCTGTATCTGGTCCAGAAGGTCCCGCACCGATTTCC  
CAGAAGTTGTCTCAATTGGAATCAAGTGACTTGGATCCACTCCCACCTCAATCCAGCGG  
TTGTAAGAATCTTTATCGTCTGGATAGTAGGTCATGTAAAGTTTTTTCAGCAGGGAAATCA  
AACCATTACAGGGCTTGTCAAAGGCTCATAAGCCCAAGTGATAGCTTCGTACGGAAGTA  
ATCCCCGATAGAGAAGTTCCCCAACATTTCAAACATGGTATGGTGACGCGCAGTCTTTCC  
CTAACGTTTTTCGATGTGCTTGGTACGGATAGCCTTTTGGGCATTGGTAATACGTGGATTT  
TCAGGGATAATGGTCCCGTCAAAGTATTTCTTAAAGGGTTGCTACCCCAGAGTTGATCCAC  
AAAAGAGTTGGGTCATTTACAGGAACCAAACCTTACTGATGGTTCTACTGAGTGACCTTTG  
GTCGCCCAGAAATCAAGCCACATTTGGCGTACTTGTGCACTAGATAGTTGTTTCATATTG  
TCTCCTTATTCACTTGTTTAATGTGATTGGCTTTCCAGTATTTCCACATAGTCAATCGCG  
ACACAGAGGGAAATGACTAGGTCTGCATAAGCGTCTTCAAGAACCGTTACGGTATAGGTA  
GAGGTCAGATGGAAGAGTTCCTTCTTAATTTCCGCAATCAACTGATCGCGATCATCCAGC  
GAATTTGAAATTCAAATCCCAGATATTGCCCTCGATACGAAGACCTAGATTATCAAACCTC  
ATACTTATCTCGCCAAAAGGTCAACTTCTTACGAATGACAAAACCTCGAGCCATCCCCAAG  
CTGAATCTCAAACGAGGAAGCAAGGTCAAGATTTCTTACTGATCTGACTGACTTGTTTC  
ACCAGCCGCATCATAGATGGTAAAAGTTTTGGGAATCTTAAAAAATGATCCCTCCACCTG  
ATAGGCAATTTCTCCCCTGTCATCCTTGATAGCGAAGCGTTCGCCTCCAAGACGAAACTT  
TTGTTTGACAAGAAATGTTTTTCATCAACACCTCCAAAAATCAAAGACAAGCTCATATCA  
CGAAGGGCGAAAAACCGCGGTACCACCTTCATTCAATGAACTTGTCATTCTCTTGTCTT  
ATGCAATTGTATGATTGAGTAGCATGACTTCCTAGCTTAGATGGCTCGCAGCACCGCCAT



TTCTCTGGACTAAGACAAGTGATATTTCCGCCAACTTGGTCAATTTACGGGTCAAGTCC  
 TCGCCTTTCTTGAGGGCACCAGGACTAGTATATGGTGGACTAGCAAAGTGAAGTGCCTCG  
 ATATCCACCCACGCTTAAGAGCAAGATAACCTGCTACAGGTGAGTCAATCCCTCCTGAC  
 AACATGAGCATCCCTTTACCTGAAGTTCCAACCTGGCAAACCACCAGCCCCACGAATGGTT  
 TCCATAAGAAAGATAGGCTGCTTCTTCCACGAATCTCCACCCTGAAGATTGATGTCCAGG  
 ACTTTTCCATTTTGAAGTTGCACATTTGGAATGGCTTCCGAATACAGCCCCCTCCA

## ORF Predictions:

ORF #	Start	End	Direction	Length
9	2812	3150	R	113 aa

[SEQ ID NO: ] 3864214-9 ORF translation from 2812-3150,  
 direction R  
 VLMKTFVLVKQKFRLLGGERFAIKDDRGEIAYQVEGSFFKIPKTFTTIYDAAGEQVSQISKEI  
 LTLLPRFEIQLRDGSSFVIRKKLTFWRDKYEFDNLGLRIEGNIWDLNFKFAG\*

## Blastp and/or MPSearch Result:

Description:  
 unknown

Assembly ID: 3864226  
 Assembly Length: 2901bp

[SEQ ID NO: ] 3864226 Strep Assembly -- Assembly  
 id#3864226  
 ATCGAATTTTATTGACAGATTAGAAAAATAATGTTACATTTATATCCGCAGGTATCTTTC  
 GATACCAAATCTACATGAAGGGACGGGGTATGAACTTTCTCATTATTTAATTGGCTTAC  
 TTCTACTCCTAGTCTTTCTCTCTATTAGCATTGGGACCAGTGATTTTTCATGGGGAAAGC  
 TATTTGATTTTCGACCAGCAGACCTGGCTCCTCTTTCAAGAGTCCCGTCTCCCAAGAACTA  
 TCAGTATTCTCCTGACTGCCTCTAGTATGAGTATGGCAGGCCTTCTCATGCAGACTATTA  
 CCAAAAATCAGTTTGCTGCACCGAGTACAGTTGGAACGACTGAAGCCGCCAACTGGGAA  
 TGGTGCTGAGCCTTTTTGTCTTTCCATCGGCTAGTCTGACCCAAAAGATGCTCTTCGCTT  
 TTGTTTCATCCATCGTATTCACCCTCTTCTTCCTAGCCTTTATGACCATTTTACTGTAA

AGGAAAGGTGGATGTTGCCTCTGATTGGGATCATCTATAGCGGGATTATCGGCTCAGTCA  
CAGAAGTTATCGCCTATCGTTTCAATCTGGTTCAGAGTATGACTGCCTGGACCCAGGGCT  
CCTTCTCCATGATTTCAGACCCATCAGTATGAGTGGCTCTTCTTAGGCCTCATCATCCTGA  
TAACCGTTTGGAAATTATCCCAAACCTTCACCATCATGAATCTAGGGAAAGAAACCAGCG  
AGAGTTTGGGGATTTCCCTACTCCCTACTTGAAAACTGGCCCTCTTTCTGGTGGCGCTAA  
CGACAAGCGTCACCATGATTACCGTGGGGGGCCTACCATTTCTCGGAGTTATCGTTCCCA  
ATCTTGTTTCGCAAGCGCTATGGAGATAATCTAAGTCAAACCAAACCTCATGGTCGCACTGG  
TTGGTGCCAATCTAGTTCTGGCTTGCGATATCCTATCCCGAGTTCTGATTAGGCCCTATG  
AGTTGTCTGTCAGTCTCTTGCTAGGAATCATCGGTAGTCTCGTCTTTATCCTACTTCTCT  
GGAGAGGGGGACGAAAAGATGCAGACTAAAAGCAAACATACCAAGCTCTTCTGGATTCTC  
ATTATTCTTGCCATCGGAGCTTGTCTTCTCTACTTTTGGCCCATCACTCACTTGTGAGCC  
TTTGCTTGGAAGTTGCGTTCCCAAAGATCATCGTTTATCTCTTGGTAGCCATCGCGACT  
GGGATTTTCGACCATTAGTTTTCAAACCCTGACGGAAAATCGCTTCCTGACGCCTAGTATT  
TTAGGAATTGAATCCTTCTACGTCTACTACAAACCCTACTACTGGTTTTTGAAAGCAAG  
TTTCTTCAACTTGGCAAATCCCCTATCTTAGAATTCCTAGTCTTACTTCTTGTCCAGTCC  
CTCTTCTTTCTCGCCTTACAAGGTTACTTGAAGACACTGATGAAGCAAGACCTGGTCTTC  
ATCCTGCTGATCTGTCTAGCGCTCAGAAGTCTCTTTCGAAATATCAGCACCTTCCTTCAA  
GTCCTAATGGATCCAAACGAATACGATAAACTGCAAAATAGTCTTTTTGCCTCCTTTCAA  
CATCTCAACACTTCCATCCTAGCCATCGGTTCTCTGATCATCCTCGCTTTGACAATCTTT  
TTCTTTTCGAAAAGCAGTCGTTCTAGATGTCTTGACCTGCAAAGAGAAACGGCTCAGATA  
TTGGGACTCGATGTTGAAAAAGAACAGAAAGAGCTCCTCTGGGGAATCGTGCTTTTGACC  
TCAACGGCCACTGCCTTGGTAGGACCTATGGCCTTCTTCGGCTTTATGCTGGCCAACCTC  
ACCTACCTGATTGTCAAAGACTATCAGCACAAGTTACTCTTTATAGTGGCCATTCTGGTT  
GGATTTATTAGCTTAACCTTGGGGCAAGCCTTGATTGAACGAGTCTTTGCACTGGAAATT  
CGTATCAGTATGATCATTGAGAGTGTGGGTGGCTTCTTATTCTTTATCTTACTATATAGG  
AGGTCTCGTCAGTGAAACTGGAAAACATTGACAAATCCATTCAAAAACAGGATATTTTGC  
AAGGCATTTTCGCTTAAAGTCAGTCCTCAAAAACCTGACTGCCTTTATTTGGTCCAAATGGTG  
CTGGAAAATCGACTCTCCTCTCCATCATGAGCAGACTAACCAAGAAAGATCAGGGAGTTC  
TCAGTATCAAAGGACGTGAAATCGAGAGCTGGAATTTCGCAAGAACTGGCTCAAGAACTAA  
CCATCCTAAAACAGAAAATCAATTACCAAGCCAAATTGACTGTTGAAGAACTGGTCAGTT  
TTGGACGTTTTTCCCTACAGCCGAGGTCGACTTAGATCAGAAGACTGGGAAAAAATCCGAG  
AAACTCTGAACTATTTGGAAGTGAACCACTTAAAAGACCGCTACATCAATAGCCTGTCAG  
GGGGGCAACTCCAGCGCGTCTTTATCGCTATGGTACTGGCCCAGGATACGGACTTTATCT  
TGCTGGACGAACCACTCAACAATCTCGATATCAAGCAAAGCGTCAGCATGATGCAGATTC  
TTCGACGACTGGTGGAGGAACTCGGCAAGACCATTTATCATCGTCCTCCACGATATCAACA  
TGGCCAGTCAGTATGCAGATGAAATTGTCGCCTTCAAGGACGGCCAGGTCTTTAGCAAGG  
GAAGAACCGATCAAATCATGCAGGCTGACCTACTCAGTCAACTTTATGAGATTCCCATCA  
CGCTAGCTGATATCAATGACAAAAAGATCTGTATCTATAGCTAGTAACATAAAAAGCTCAA  
GTTAGAGAACCTTCAGTCTCTTAGTCAATAAGATCAAGAGACTCCCTAAATCGTTATCAC  
ATTTTAAAAAGGAGAAATTATGAAAACATCCCTTAAACTTTATTTCACTGCCCTAGTGGC  
CAGCTTCTTGCTCCTACTTGG

## ORF Predictions:

ORF #	Start	End	Direction	Length
8	1992	2744	F	251 aa

[SEQ ID NO: ] 3864226-8 ORF translation from 1992-2744, direction F

VKLENIDKSIQKQDILQGISLKVSPQKLTAFIGPNGAGKSTLLSIMSRLTKKDQGVLSIK  
GREIESWNSQELAQELTILKQKINYQAKLTVEELVSFGRFPYSRGRLRSEDWEKIRETLN  
YLELTNLKDRYINSLSGGQLQRVFIAMVLAQDQDFILLDEPLNLDIKQSVSMMQILRRL  
VEELGKTIIVLHDINMASQYADEIVAFKDGQVFSKGRTDQIMQADLLSQLYEIPITLAD  
INDKKICIYS\*

## Blastp and/or MPSearch Result:

## Description:

ECFHUACD NCBI gi: 4143 - Escherichia coli. (fhuC, ferric enterobactin transporter ATPase, ABC type)

Assembly ID: 3864242  
Assembly Length: 1930bp

[SEQ ID NO: ] 3864242 Strep Assembly -- Assembly id#3864242

CGANGGCCTTGATCTGGTGATGAAAAACAAGAATTGACTGCTGAAACTATCGTCATCAAC  
ACTGGTGCTGTTTCAAACGTCTTGCCAATCCCTGGACTTGCTACAAGCAAAAACGTCTTT  
GACTCAACAGGTATCCAAAGCTTGGATAAATTGCCTGAAAAACTTGGAGTCCTTGGTGGC  
GGAAATATCGGTCTTGAATTTGCTGGCCTTTACAATAAACTAGGAAGCAAGGTTACAGTC  
CTAGATGCCTTGGATACATTCCTACCTCGTGCAGAACCTTCCATCGCAGCTCTTGCTAAA  
CAATACCTGGAAGAAGACGGTATTGAATTGCTTCAAAAATATCCATACTACTGAAATTAAA  
AACGACGGTGACCAAGTGCTTGTCGTAAGTGAAGACGAACTTACCGTTTCGACGCCCTT  
CTCTACGCAACTGGACGCAAACCAATGTAGAACCCTTCAACTTGAAAATACAGATATT  
GAACTAACTGAACGTGGCGCTATTAAAGTAGATAAACACTGTCAAACAAACGTTCTGGT  
GTCTTTGCAGTTGGAGATGTCAACGGTGGTCTTCAATTTACTTACATTTCACTTGATGAC  
TTCCGTGTTGTTTACAGCTACCTTGCTGGAGATGGCAGCTACACACTTGAGGACCGTCTC  
AATGTACCAAATACTATGTTTCATCACACCTGCACTTTCACAAGTTGGTTTGACTGAAAGC

CAAGCAGCTGATTTGAAACTTCCATACGCAGTGAAAGAAATCCCTGTTGCAGCCATGCCT  
 CGTGGTCACGTAAATGGAGACCTTCGCGGAGCTTTCAAAGCTGTTGTTAATACTGAAACA  
 AAAGAAATTCTTGGTGCAAGCATCTTCTCAGAAGGTTCTCAAGAAATCATCAACATCATT  
 ACTGTTGCTATGGACAACAAGATTCCCTTACACTTACTTCACAAAACAAATCTTCACTCAC  
 CCAACCTTGGCTGAGAACTTGAATGACTTGTTTGCGATTTAAGTTGAAATCTCATCTTAA  
 CTGACAGCCCTCTTTGGGCTGTTTTTACTTCTACGAAACACCAAATCTGTCTTTTCCCTC  
 TTTTGTGATATAATAGAAACATGAACTTAAAACTACTTTGGGCCTTCTTGCTGGGCGTT  
 TCTTCCCACCTTCGTTTTTAAGCCGTCTTGGACGTGGAAGTACGCTCCCAGGGAAAGTCGCC  
 CTTCAATTTGATAAAGATATTTTACAAAACCTAGCTAAGAACTACGAGATTGTCGTTGTC  
 ACTGGAACAAATGGAAAAACCTGACAACCTGCCCTCACTGTCGGCATTTTTAAAGAGGTT  
 TATGGTCAAGTTCTAACCAACCCAAGCGGTGCCAACATGATTACAGGGATTGCAACAACC  
 TTCCTAACAGCCAAATCTTCTAAAACTGGGAAAAATATTGCCGTCTCGAAAAATTGACG  
 AAGCCAGTCTATCTCGTATCTGTGGACTATATCCAGCCTAGTCTTTTTGTCATTACTAAT  
 ATCTTCCGTGACCAGATGGACCGTTTCGGTGAAATCTATACTACCTATAACATGATATTG  
 GATGCCATTTCGGAAGTTCCAACCTGCTACTGTTCTCCTTAACGGAGACAGTCCACTTTTC  
 TACAAGCCAACCTATTCCAACCCCTATAGAGTATTTTGGTTTTGACTTGGAAGGACCA  
 GCCCAACTGGCTCACTACAATACCGAAGGGATTCTCTGTCCTGACTGCCAAGGCATCCTC  
 AAATATGAGCATAATACCTATGCAAACCTGGGTGCCTATATCTGTGAGGGTTGTGGATGT  
 AAACGTCCTGATCTCGACTATCGTTTGACAAAACCTGGTTGAGTTGACCAACAATCGCTCT  
 CGCTTTGTCATAGACGGCCAAGAATACGGTATCCAAATCGGCGGGCTCTATAATATCTAT  
 AACGCCCTAG

## ORF Predictions:

ORF #	Start	End	Direction	Length
6	376	1002	F	209 aa

[SEQ ID NO: ] 3864242-6 ORF translation from 376-1002,  
 direction F

VLVVTEDETYRFDALLYATGRKPNVEPLQLENTDIELTERGAIKVDKHCQTNVPGVFAVG  
 DVNGGLQFTYISLDDFRVVYSYLAGDGSYTLEDRLNVPNTMFITPALSQVGLTESQAADL  
 KLPYAVKEIPVAAMPGRGHVNGDLRGAFKAVVNTETKEILGASIFSEGSQEIIINIITVAMD  
 NKIPYTYFTKQIFTHPTLAENLNDLFAI\*

## Blastp and/or MPSearch Result:

## Description:

UNKNOWN DEHYDROGENASE A (EC 1.-.-.-). - ESCHERICHIA COLI.

Assembly ID: 3864254  
Assembly Length: 2674bp

[SEQ ID NO: ] 3864254 Strep Assembly -- Assembly  
id#3864254

CTACTGCTTGTTTGATAAAGTCCTGAATCGGCTCTCCTTGGTGGAGAGCTTTTACTATTT  
TCGAACCGACGATAACACCATCTGACACCGCATTGAAGCGTTCAGATTGGCTTGACTAG  
ATACACCAAAACCTGTCAAGACTGGGATGTCGGCCACTTGATGAAGTTGCGCCAAGTGCT  
TGTCCAAATCTGCATCGGTAATTGCCTGATTTCCCTGTTACCCCATTGATGGCAACGGCA  
TAGACGAATCCCTCCGCCCCCTCAATCAACTCTTTCTGGCGCTCAATTCCTGTGGTCAAG  
CTTACTAAAGGAATCAAGGCGATATCTGTATCTGCCAAAAATGGTCTACAAAGTTGGCA  
TGTTTCATGAGGCAGGTCTGGGATAATCAAGCCCTTCACAGCTGTATCAGCCAGATCTTTG  
ACAAAGTTCTCCACACCGTACTGAAAGAGGGGGTTGAAGTAGGTCATGATGACCAGTGGA  
ATCTCTGTTTCAATGGTTCCTCAAGGTTCAACTAAAGCCTGGGTAGAGGTCCCGTGGGCT  
AAACTGCGCAAGCCAGCTTCTTCAATAACAGGTCCATCTGCAACAGGGTCTGAAAAGGGA  
ATACCCACTTCAATAGCAGAGACACCCAAATCTTCTAAAAAGTGAATTGTTTCAGCAAGA  
CCGTCCAAACCTTTTTCGTGGTCAACAGCCATGATATAAGGAACGAAAATTCCCTTTTCCA  
GTTGCTTTTATAGCATTCAATTTTTCTGTAGTGTCTTAGGCATGAGCTTCTCCCTTCTT  
TGCTGCATCTGCTTCCAAGCGGTCTTTGACTTGAACCACATCCTTGTCACCCACGACCTGA  
TAGGCAGACAATCATAGACTTTTCTGGTCCAAGTTCCTTTGGCCAATTTACCCGCAAAAGC  
GATAGCATGGCTAGATTCCAAGCTGGGATAATCCCTTCCACACGAGACAAGAGTTGGAA  
TCCTTCCAAGGCTTCTTCGTCTGTACAGGGACATAGCTGGCACGTTTAATATCGTGGTA  
GTGAGAAATGCTCTGGACCGATACCAGGATAGTCCAAACCTGCTGAGATAGAGAAGGCTTC  
AAGAATTTGACCATGGGCATCTTGGAGCACATCCATGAGGGAACCGTGAAGGACACCTGG  
ACGACCCTTGGTCAAGGTAGCTGCGTGGTGCTCCGTATCCACACCAAGTCCAGCCGCTTC  
AGCTCCATACATGGCTACAGACTCATCTTCTACAAAGGGATGGAAGAGCCCAATAGCATT  
AGATCCACCACCAACACAGGCTACTAGGGCATCGGGCAGATTTTGACCTGTCATATCGCG  
ATACTGTTGTTTAGCTTCGCGACCGATGACACTTTGGAAGTCACGAACGATTTCTGGAAA  
TGGATGAGGCCCCAAGGCAGAACCAAGGATATAGTGGGTATCGTCGATATTAGCCACCCA  
TGAACGAAGGGCTGCATTGACCGCATCCTTGAACACGCGCGAACCATCTGTCACTGCCTC  
AACCTTAGCTCCCAAAAGCTCCATACGGAACACATTGAGGGCTTGGCGTTTGACATCTTC  
CTCACCCATGTAGATGGTACATTCCATGTTAAAGAGGGCCGCAGCAGTTGCAGTTGCCAC  
ACCGTGCTGACCAGCACCCGTTTCTGCGATAATTTTCTTTTACCCATGCGTTTGGCAAG  
CCAAACTTGTCCTAAGGCATTGTTAATCTTGTGGGCTCCTGTATGGTTAAGGTCTTCCCG  
TTTGAGATAAATCTTGGCTCCGCCGATATGCTGGGTCAAGTTTTTTGCGTAGTAAAGAGG  
AGTTTCACGTCCTACGTACTGGCGCAAGAGTTGGTTTAATTCCTCTTGGAACCTTGGGTC  
TGCCTGACTTTTACGGTAGGCCTTCTCCAACCTCCAAAACTGCTGTCAATGTTTCTGG  
GACAAAACGTCCGCCGAATTTTCCGTAAAATCCATCTTTATTTGGTTTCTGATATGCCAT  
GCTTTACCCTCTCTATAAATCTTCTAATCTTTTCATGATCTTTTTGTCCATCTGTCTCCA

CTCCGCTCGATACATCTACTGCATAGGGAGTAAAATGTTGAATTGCTTTTACTACATTAT  
 CTTTCATTAAGGCCACCTGCGATAAAGAAGGGCTGTGCTAGTCCAGTCGTATCCAGTTGAC  
 CCCAATCAAAGGACTGGCCACTTCCTGCCACAGGGGCATCAAAGAGTAGATAATCTGCCT  
 GAGAATTGGGGACATGCCCCATTTCCATCTACCTGCACAGCCTGAATACTGGCACAAGGCA  
 AATTCTCAAATAAATCATCTGCCACCTGACCGTGAACCTTGAACCAAGTCCAAGCCAACTT  
 TGTCAATCGCTTCCAGCAGTTCTACCCGACTTGGTGAAACAAATACTCCAACCTTTTTTCA  
 CATCTGCAGGAATAAGCTTTGCCAACTCAGCTGCCTCTTCTAAAGTCACCTGTCTTTTAC  
 TAGGTGCAAAGACAAAACCGATATAGTCGGCTCCTGCTGAAACGGCTGTTTCCACCGCTT  
 CTTTGGTCGATAGTCCACAAATTTTAACCTTTGTCAATCTGCAACTCCTTGATTCTCTGG  
 GCCACATTTTCTGCCTGCATAAGAGCTGTCCCTACCAAAATTCGGTTAAAGTATGGGGCT  
 AGTCGTTCCGCATCCTGCCCTGTGAAAATGGCAG

## ORF Predictions:

ORF #	Start	End	Direction	Length
6	117	833	R	239 aa

[SEQ ID NO: ] 3864254-6 ORF translation from 117-833,  
 direction R

VGTRMWFKSKTAWKQMQRREKLMPKTLTEKLNAIKATGKGIFVPYIMAGDHEKGLDGLA  
 ETIHFLLEDLGVSAIEVGIPFSDPVADGPVIEEAGLRSLAHGTSTQALVETLKTETEIP  
 L VIMTYFNPFLFYGVENFVKDLADTAVKGLIIPDLPEHANFVEPFLADTDIALIPLVSLT  
 TGIERQKELIEGAEGFVYAVAINGVTGKSGNYRCRFGQALGATSSSGRHPSLDRFWCI\*

## Blastp and/or MPSearch Result:

## Description:

TRYPTOPHAN SYNTHASE ALPHA CHAIN (EC 4.2.1.20). - LACTOCOCCUS  
 LACTIS (SUBSP. LAC TIS) (STREPTOCOCCUS LACTIS).

Assembly ID: 3864296

Assembly Length: 3074bp

[SEQ ID NO: ] 3864296 Strep Assembly -- Assembly  
 id#3864296

CCAACATTACATGTTCCAATTTTCTCTGGTTTGGCTTGTGTAGTTAACAAATACATAA  
TCTACACCTGTCAAAACGATGAAGAGGTCTGCATCAACCAATTCTGCCAAACGTTGGGAA  
GCGAAGTCTTTATCAATAACCGCTTCGACACCAGTCAAATGTCCATTGTTTTCTTTGACG  
ACGGGAATACCGCCACCACCTGCAGCTACGACGACTTGACCATTATTTAAAAGAGTACGG  
ATGGTTTCAATTTCTTTGATATCAACAGGTTTTGGTGAGGCAACGACCTTACGCCAGCCA  
CGGCCAGCATCTTCCTTGAAAGTCGCTCCGCTCTTTTCGGCTTCTGCTTTTGCTTCTTCT  
TCTGAATAGAAAGGACCGATTGGTTTACTCAAGTTAACAAAAGCCGGATCATTTTTATCT  
ACGACAACCTTGCCTTACAACAGAAGCAACATTTTTTTTCGATGCCCTTCATCCAAGAGAGCA  
TTTTGCAAAGCATTTTTCAACCAGAAACCGATGCTACCTTCTGTCATAGCGACAAGTGAG  
TCGAATGGGAAGGCAGGGTTCCTTTTCAGAGTTCTGATGCCAAATGTTTGGAGCAAGAGA  
TTCCCAACTTGAGGTCCCATTACCGTGAGTTGATAATCAAATCATCTCCATTTTTAATCC  
AATTTTACAAGATGCTTAGCTGTTTCAACTAAAGCTTCCTTTGTTGAGCCCTTTGCTGAT  
GGGTCAGAAGAAAGAATCGCATTTCTCCCAAAGCTACTACAATTTTACGATTTGCCATA  
AATCTCCTTTATCACACTCAATAGAATGCGTTTAGATTTCAATTTAATGATTTTTTCACA  
TATTTTATAAGAAATAATAGATTACCATTATATAAAAGAGGACCGGACTAAAGCTATTAG  
TCGCAGCCCTCATAGCTGTTGGTAGACGGTTTATTATCTAAAATTATACTTTAGGAATAT  
AAAGGTTACCAAGTGTAGCAGCCATAACAGCTTTGATAGTGTGCATACGGTTTTCTGCTT  
GATCGAAGTGGCGAGCGTACTTGCTGCGGAAGACTTCGTCTGTTACTTCCATTTCTTCTA  
CACCAAATTTTTTCAGCAACGTCTTTACCATAAACAGTGTGAGTATCGTGGAATGCTGGCA  
AGCAGTGTAGGAAGATCAAGTTTTTCATTGCCTGCTTTTTTAACTAAGTCCATATTGACTT  
GGTAAGGTTTAAAGAAGAGCTACACGTTCTGCGAATTTGTCTTCTTCACCCATTGATACCC  
AAACGTCTGTGTAAAGAACGTCTGCATCTTTAACTGCTTCATCAGCATCTTCAGTGATGA  
GAACATGTGCGCCACTTTCTTTAGCAAATCCTTCTGCCAATTC AACGATTTCTTTTTCTG  
GGAAGAGTTCTTTTGGTGAGAAGATGTGAACATTGACACCAAGGATAGCACCTGTTACGA  
GCAAGCTGTTGGCAACGTTGTTACGTCCATCACACAGTATACCAATGTCAAGCCTTCCA  
AGCGACCGAAGTTTCTTGAACAGTCAAGTAGTCAGCGAGCATTTGAGTTGGGTGCCATT  
CGTCAGTTAGACCGTTCCATACTGGAACGCCTGAGAATTCTGCCAATTCTTCAACCATAA  
CGTTGGCTGAATCCGCGGAATTCAATCCCGTCAAACATACGTCCCAATACTTTAGCAGTA  
TCTTCAGTAGATTCTTTTTTACCCAACTGAATATCATTTGCTCCGAGGTATTCTGGGTGA  
GCACCAAGGTGATAGCCGAGTTGTAAAGGCTGCACGAGTACGAGTAGATGTTTTTTCA  
AATAGGAGAGCGATATTCTTGCCAGCAAGGTAGTGGTGTTGAATATTGCGTTTTTTTCAA  
TCTTTCAAGTGAGCTGAAAGACCAATAAGGTATTCTAACTCTGCACGGGTAAAGTCTTTT  
TCTGCTAAGAAGCTGCGTCCTTGGAATACTGAATTTGTCATTTTATTATTCTCTCTTCT  
ATTTTTTACATTTTCTATTGACGAATGCCGAACAGCGATTACACTTCTTCACGTTCAAAT  
GGCATAGACATAACAACGAGGTCCACCACGGCCCCGAACCAATTCACCTCCGCGAATCTTA  
ATCAAGCGAAGCCCGTATTCTTCCAAAATCTTATTGGTCACGGTATTGCGGTCATAAACA  
ACTACCACACCAGGTGCGATGGTCAAAGTGTTAGAACCGTCGTCCCATTGTTTCACGCGCA  
GCTGCTACGATATTGCCACCACCGCAACGAATCAAATGAACTTTTTCTACACCAAGGTTT  
TGAGCAAGAAGTTCAGCTAAGTCACCTTTCTCTTCAACGATTTTAAAGTTTTTCGTTTTCG  
TAAGTAACTGAGTAAAACGTGAAGGTCGCCTTCGATTTCTGGGTGAATAGTGAACCTTGTC  
ATAGTCTACCATAGTGAAGACAGTATCCAAGTGCATGAATTTACGGTTGTTAGCAAATTC  
AAAGGCCAAAACCTTTCTTGAAGCCAACATTTTTCTTGAAGATGTTGACCAAAAGTTTTTC  
GATAGAAGCTGCGTCTGTACGTTGAGAGATACCTACTGCAAGGACGTCTTTAGAAAGAAC

TAGCCTCGTCTCCACCTTCGATACGCGTATCTTCTTCACGGTTGTAGACCAAATCCACTT  
 TTCCGCCATAGATTGGGTGGTATTTGAAGATATACTTACCGTAGAGTGTTTCACGGTTAC  
 GAGTGTCTGCAAACATGTGGTTAAGCGATACGGCGTTTCCAATTGTTGCAAATGGGTCGC  
 GAGTGAAATAGAGGTTTGGCATCGGGTCAATTGCAAATGGATAATCTGATTCAACTAAGT  
 CAGTTAGATCTTTAGCTTCGTCAGGAATTTCTGGCAATTCAACTTTTTGAATCCCAGCCA  
 TTGTTTTTTCAACCAATTCCTGGTTGTCCTTGATGCCGTGAAGCAATTCACGAATAGCAA  
 CCTTGGTTTGACGATCACGGATGTTGGCTTCGTCTAAGTATTCCTCGATAAATTGATCGC  
 GGATTTCTGGAGAAGTCCAATGAATCCAGCAGCGAGTTGTTCTACCTCCAGAACCGATTA  
 TCTGCTGTTTCGAG

## ORF Predictions:

ORF #	Start	End	Direction	Length
7	944	1777	R	278 aa
10	2323	2694	R	124 aa

[SEQ ID NO: ] 3864296-7 ORF translation from 944-1777,  
 direction R  
 VQPLQLRLSTLVLTQNTSEQMIFSWVKKNLLKILLKYWDVCLTGLNSADSANVMVEELAE  
 FSGVPVWNGLTDEWHPTQMLADYLTQENFGRLEGLTLVYCGDGRNNVANSLLVTGAILG  
 VNVHIFSPKELFPEKEIVELAEGFAKESGAHVLITEDADEAVKDADVLYTDVWVSMGEED  
 KFAERVALLKPYQVNMDLVKKAGNENLIFLHCLPAFHDTHTVYGKDVAEKFGVEEMEVD  
 EVFRSKYARHFDQAENRMHTIKAVMAATLGNLYIPKV\*

## Blastp and/or MPSearch Result:

## Description:

ornithine carbamoyltransferase (arcB) homolog - Haemophilus  
 influenzae (strain Rd KW20)

[SEQ ID NO: ] 3864296-10 ORF translation from 2323-  
 2694, direction R  
 VKHSTVSISSNTTQSMAEKWIWSTTVKKIRVSKVETRLVLSKDVLAVGISQRTDAASIEK  
 LLVNIFKKNVGFKKVLAFEFANNRKFMHLDTVFTMVDYDKFTIHPEIEGDLHVLLSYLRK  
 RKT\*

## Blastp and/or MPSearch Result:



## Description:

STREPTOCOCCAL ACID GLYCOPROTEIN. - STREPTOCOCCUS PYOGENES.

Assembly ID: 3864300

Assembly Length: 3205bp

[SEQ ID NO: ] 3864300 Strep Assembly -- Assembly  
id#3864300

GGGGGCCAAAGCCAAAAGACTTCAAATAGCTAGAACCTACTTAAAAAGATGCTGAAATTCT  
TATATTTGATGAAGCCACTGCTAATCTTGATGCGGATTCTGAGTATGCGATTATCAGTAG  
CCTCTATTCTGTATTAAAGGAGAAGACGGTTGTGATTATAGCGCATAGTTTGTCAACGGT  
AAAAGATGTGGATTGTATTTTCTTCTTAGAGGAGGGGAAAATCACTGGCTCAGGAACTCA  
TAAGGAACTACTGGAAAATCATGAGCGTTATGCTCGTTTTGTGCAGGAGCAAATGATAGA  
GTGAAGTGTCTTTTGAGATTCACCATTTTATAGTCTATTAAAGGGAGCAGGAAAACTCC  
CTTTTTATATAGTTTGAAACTATAACTAGCTCTTGAAAAGAAGAAAATGAGTTGATGAAA  
ATAAGTGGTACAATAGTTACTATAGATTTGGAGGTATTGTATGAGCAAGGAATTACACAT  
TAACACAATTTTGGCCCAGGCGGGTATTAAGTCAGATGAAGCGACAGGTGCATTGGTGAC  
ACCGCTTCATTTTCAACGACCTATCAGCATCCAGAGTTTGGTCGATCTACTGGGTTTGA  
CTATACGCGCACTAAAAATCCAACCTCGTAGTAAGGCTGAGGAAGTCTTGCGCGCTATTGA  
GTCAGCAGACTATGCCTTAGCGACTAGCTCAGGGATGTCAGCTATTGTACTGGCCTTTAG  
CGTCTTTCCAGTAGGAAGTAAGGTCTTGGCAGTGCGTGATCTTTACGGTGGTTCTTTTCG  
CTGGGTTTAAACCAAGTGGGAGCAGGGAAGGTCTTTCCATTTTAACTATGCCAATAACA  
GAAAGGAAGAGTTGATTGCCGGAGTTAGGAAAAGGATGTGGATGTTCTCTATATCGGAAA  
ACCCCAACCAATCCCTTGATGTTGGAATTTGATATCGAAAACTAGCAAAATTGGCTCAT  
GCTAAGGGTGCCAAAGTGGTGGTGGACAATACCTTCTATAGCCCTATCTACCAACGTCCG  
ATTGAAGATAGAGCAGATATCGTTCTCCATTCTAGCAACCAAGTATCTAGCAGGCCACAAT  
GATGTCTTGGCTGGAGTGGTTGTGACCAATAGTTTAGAACTATACGAGAAGCTTTTTTAC  
AATCTCAATACAACAGGGGCAGTCTTGTCTCCATTTGACAGCTACCAAGTTGCTTCGTGGT  
CTCAAGACCTTGTCTCTTCGTATGGAGCGTTCAACAGCTAACGCCCAAGAAGTGGTTGCC  
TTTTTTGAAGGATTCTCCAGCAGTTAAGGAAGTTCTCTACACTGGTCTGGAGGCATGATT  
TCCTTTAAAGTAGCCGATGAAACACGCATTCCTCATATTTTGAACAGTCTCAAGGTCTTC  
TCTTTTGCAGGAAAGTTTGGGCGGAGTGGAAGTCTTATTACTTATCCAACGACTCAAAC  
CATGCTGATATTCCAGCAGAAGTACGCCATTCTTATGGTTTGACAGATGACCTCTTGCGT  
TTGTCTATTGGGATTGAGGATGCTAGAGATTTGATTGCAGATTTGCGCCAAGCCTTAGAA  
GGATAAGACAAAGATGGGAAAATATGATTTTACAAGCCTGCCCAACCGTTTAGGGCACCA  
TACCTATAAATGGAAAGAAACAGAAACGGATAGTGAAGTTCTACCAGCTTGATAGCGGA  
TATGGACTTTGTGGTCTTGCCGTGAAATCCGCCAAGCCGTGCAAACCTTACGCAGACCAACT  
GGTTTATGGTTATACCTATGCCAGTGAAGACTTAATTAAGGAAGTTCAAAGTGGGAAGC

TACACAATACGGTTACAACCTTTGACAAAGAGGCTCTTGTCTTTATCGAGGGTGTGGTACC  
 AGCCATCTCAACAGCTATTCAAACCTTTACAAAAGAAGGCGAGGCGGTTTTAATTAACAC  
 GCCTGTCTACCCACCCTTTGCTCGCAGTGTCAAGTTGAATAATCGTAGATTGATTACTAA  
 TTCCTTAGTGGAAGGATGGTCTGTTTGAGATTGACTTTGACCAACTTGAAAAGGATTT  
 GGTGGAAGAGGAGGTAAACTCTATATTCTTTGCAACCCTCACAATCCTGGTGGACGTGT  
 TTGGGAAAAAGAAGTGTGGAGAAGATTGGCCAACCTCTGCCAAAAACACGGTGTTTTGT  
 AGTTTCGGATGAGATTCACCAAGATTTGACCCTCTTTGGTCACAAACACCAGTCTTTCAA  
 TACCATCAATCCTGCCTTCAAAAATTTTGCTATCGTCTTGAGCAGTGCCACTAAAACATT  
 TAATATTGCTGGAACAAAAAATTCCTATGCAGTCATTGAAAATCCTAAGTTGAGACTAGC  
 TTTCCAGAAACGCCTGTTGGCCAATAATCAGCATGAAATTTTCAGGCTTGGGTATTTGGC  
 GACAGAAGCTGCCTATAGATACGGTAAAGATTGGCTAGAGGAACTCAAGCAAGTCTTTGA  
 AGACCACATCAATTCGATGTGGTGGATCTATTTGGAAAAGAGACTAAAATCAAGGTCATG  
 AAACCGCAAGGTACCTACTTGATTTGGCTTGACTTTTCAGCCTATGACCTGACTGATGAA  
 ACATTGCAAGAGTTGTTGAGAAATGAAGCCAAGGTATCCTCAACCGTGGTTTGGATTTT  
 GGAGAGGAAGGAAGTCTCCATTCCCGCATCAAGATTGTTAGCTATGCCCAAATCTCTGTT  
 GCAAGAAGTCTGTGACGGATTGTGGCTACTTTTGCCAAACGTTAAAAATCCAGCCTTCT  
 AGGAGAAAAGTCTTCCTAGAAGGCTATTTTCATAGGCGAAAATATGGTATAATAAACAGA  
 TAAGGTAAAGGTGAAAATATGGCTAAATTGATTCCGGGGAAAGTTTCGTATCGAAGGTGTT  
 GCCCTTTATGAAACTGGTAAGGTTGATATCATCAAGGAAAAGAACAATCGGCTCTACGCT  
 CGCGTTGCAAAGAAGAACTGCGCTATAGTTTAGAGGATGATTTGGTTTTTTGTGCCTGT  
 GATTCTTTTCAAAAGAGGGGCTACTGTGTGCATTTGGCAGCGCTAGAGCATTTTCTGAAA  
 AATGATGAGCGTGGTCAGGAAATCTTGTGGAGTCTGGAAGAAGGTCATGAAGAAAAAGAG  
 GCCGTTGAAACCAAGGTGACCTTGGGTGGCAAGTTTTTTGAATCGAATTTTATCTCCGAAA  
 TCAGAATGCGCCTATGAGTTATCAG

## ORF Predictions:

ORF #	Start	End	Direction	Length
9	2479	2823	F	115 aa

[SEQ ID NO: ] 3864300-9 ORF translation from 2479-2823,  
 direction F

VVDLFGKETKIKVMKPQGTLYLIWLDF SAYDLTDETLQELLRNEAKVILNRGLDFGEEGSL  
 HSRKIVSYAQISVARSLSADCGYFCQTLKIQPSRRKVFLEGYFHRRKYGIINR\*

Blastp and/or MPSearch Result:

Description:

PUTATIVE AMINOTRANSFERASE B (EC 2.6.1.-) (FRAGMENT). -  
BACILLUS SUBTILIS.

Assembly ID: 3864312  
Assembly Length: 1665bp

[SEQ ID NO: ] 3864312 Strep Assembly -- Assembly  
id#3864312

AATTGATGGCGCATATAGGCTTCCATGGACCTTGCTTTTTTAGAGTCTTTTGCTGCTTCT  
AGCTCCTCAAGTAAATCTGCTAAACTCATCTAAACTCCTCTTGCCCCACCAAATGGTG  
TGAAAGGCATACACAGTCGCCTGGGTACGATCGCTGACTTCAAGTTTGGCAAGAATATTG  
GACACGTGGGTCTTGACCGTCTTGAGAGAGATAAAGAGGTCATCTGCGATGCGCTGATTT  
TCGTAGCCCTTGGCGATGAGTTGGAGAACATCTCGCTCACGCGCAGTCAATTCTTCATGA  
AGTTCCATATGATTGCGGTGGTATTCAACCTTCTTGCTAACCTCTTGCTCAATGGCCAGC  
TCGCCAGCAGCTACCTTACTGACGGCATGAAGCAATTCATCTGCACTAGAAGTCTTGAGC  
ATATAGCCTTTGGCACCAGCATCTAAGACTGGCATGATTTTTTTCATTGTCCAAATAAGAG  
GTCACAATCAAAATCTTGCTTCAGGCCATTCTTTAAGGATTGCTAAGGTCGCGTCAATC  
CCATTTCATCTCAGGCATGACAATATCCATGACAATGACATCTGGACGCAGTTCCAAGGCC  
AAGTCAATCCCTTGAGACCCGTTGGACGCCTCACCCACAACCTTCTACATCGTCTTGAGG  
TCAAAGTAGCTTTTCAAGCCCAATCGGACCATTTCATGGTCATCTACTAGTAAATTTTC  
ATCTTTACTCCTTTATCATTCCTTATCTAACAGGGGAATACGGATATCAACTGCCAGCCC  
TTGCTTGGGAGCTGTTAATAACTGAACCGTCCCTGCCATATCTTCAACCCGCTCCTTGAT  
ATTTTCGCAGTCCATAACTCAAGTCGTCTAAGCTCCCTAACCGGAAACCAATCCCATTTGTC  
CACCACCTTCAGTTGCAATTCAACATCTGTCTGATAGAGGTAGACATCTAGGCAAGATGC  
CTGGGCATGGCGGAGCGTATTGCTAATCAACTCTTGCAAGGATACGGAAGATATGCTCCTC  
GATTTTCTTATCGGCAATTTCTGCATATTCTGCTTGAGACTAACCCTAAGATCACTCTTG  
TCCTCAAGCTCTTTTAAGAGAATCTGAATCCCTTCTATCAAGCTCTTCTGCTCCAGTTCA  
ACTGGTCGCAAATGCAAGAGCAAAACCCGCAAATCCTTCTGGGCAGTTTCTAAATAGCT  
GTGACACTCTGCAACTGGATCTGCATCTTTTCTCTATCCAATTTCAAAGCCTGCTGACTG  
ATACCCGATAAAATCATGTGGGCCGCAAACTCCTGACTGACTGTATCGTGCAAATCC  
CGAGCAATTCGCTTCCGTTCTTTCTCGATGATTTCTCTCCTTGAGCAAGGCTATGATTT  
TCAGCTTTTGAAGAGCTTCTGTCAAAGGTTAAGTTTACCTGATAAGGACTTGAACTG  
GCATCCAAATCTGGATCTGCAACCTGAACCACTTCTTGCCCTGCCAATAAACGCTTGAGA  
TTAGCCTGCATTTTCTTAGAGAAAGCTCTTCGATCCCTCGCCAAAACAGGGCTAAGAGA  
CAGGTTATGGACATGCTGAAAACCAACAATAAAAAGACAAATTTTCTGTTTTTTCGACA  
TCGTGCAAAAAGATAGACCAGTCAAAATCAAGTATTTCCAGCAAG

ORF Predictions:

ORF #	Start	End	Direction	Length
7	736	906	R	57 aa

[SEQ ID NO: ] 3864312-7 ORF translation from 736-906,  
direction R  
VVDNGIGFRLGSLDDLSYGLRNIKERVEDMAGTVQLLTAPKQGLAVDIRIPLLDKE\*

Blastp and/or MPSearch Result:

Description:  
unknown

Assembly ID: 3864336  
Assembly Length: 2532bp

[SEQ ID NO: ] 3864336 Strep Assembly -- Assembly  
id#3864336  
CTGAGTGAAGAAAAGTACCACCACGAGAAATGATGTCTCCTACTGAAGCTGCATCTAGGG  
GATGAATTTACCGGCAACCATACCAGCATATCCGTCATAGATACCAAACACTTCCATTC  
CTTCTGAAATTGCTTGACGAACAACTGCACGGATAGCAGCGTTCATACCAGGTGCGTCTC  
CGCCACTAGTCAAAACAGCAATACGTTTCATATTGGTTTATGCTCCTTTTTCTTTTAAACA  
TTCTTTCTTGATTATATCACATTTGATTTTAAATCTTCTATTTTCCGTATTTTAGCG  
ATAAATCGTTTTTCATAACGATTTTCATTCAATTTCTCCTCTAATTCATTGGATTTAGCTAC  
AAAATGATGGGGAGAAACGATGGTTTTCTGTTCTCTTCATACCAGGATGATGACTGGGAT  
TGGGCCTTTAAATTGTTCTAAAATACGTGAAATTTCTTGATCCGATTCATGATTTTTCAC  
CTGTATCCAAAAGCGTTCAGCAACTGCTTCTCTTATTTCTTGTCGAATCATTTGCAAACG  
GCCATCACGTGATTGTATTTTTCCTTTTACATAGTAGAAGGCTCCCTCTTTTATTTCCCTG  
TCCAACCTGACGATATAAGTCTGAAAAGAGAGTGACATCCAATTTTTTCTTACTATCATC  
TGCCTGTAAGAAGGCCATATTTTCACCCTTTTGGTACGAATCACTTTTATTTTCTGAAC  
TTCAACCAAATAATAGCATAGCTATTTTCTGACAAATTTCCGATTGGGGTAATCGGGTA  
AATAGCCTTACTTGCAATAGCTTGAGNGGATGTATGCTGACACCTATCCCTAAAAGCTC  
TTGTTCCATATAAAATTTTTCTTGTTCCGTCCAATCTTCCGATTCCTGCCAACTATAAAT  
AGCATCTCCAAACAACTTCCCAACTCTTTCACAAATTCAAATAGATTAGCTAAGTTATT  
AAATACTTTTTGACGATTTTTTTCAAATGAATCGAAAAGACCAACTTTTACCAAAGGTTTC  
TAGCAGAGGAAGTTTCAGATAATTCTCAGGTAATTTAGCTATAAAATCTTCAATGTTAGA

ATAAGGTCTATGTTCAATAATCCAAAGCGCCAAGTCCTTGCTGAGCCCCCTTAATCGATTT  
CAAACCTATATAGATAGACTTGTTGGCAATTTTATCGTGATAGGGAATAGTATTGATGGA  
TAGAGAGGCTACTTCAAACCTGCTTCAAGTGCATCTATTAAGTAATCACTGTTGGAATA  
ATTTAACATGACCTGATAAAAAATGGCTGGATAATGCGTTTGTGAAATAAGCCAACTGGAA  
GGCCAAGGCTGAGTAGGCGTAGGCATGAGATCTATTAAATCCATAACCTGCAAACCTTCTC  
CATAACATCAAAAACCTGCTCTGATTTTTCCGCGAGTATGGCCTGCTTCTATGGAGCCTTG  
AATAAAGGAAGCCCTCATCTCATGCATAGCAGAGGCATCCTTTTTTACCCATAGCTCGACG  
CAAAATATCGGCCTTCCCAAGACTAAATCCAGCAAATCGCTGAGCAACCTGCATAACCTG  
CTCCTGATAGAGCATAATGCCATAAGTTGGAGCCAAAATATCCTCCAGAGCTGAATCTAG  
AACAGTCACTTCTTCCCTGCCCATGCTTCCTTGCCACAAAATTATTGATGTAGTCACTTGC  
ACCTGGTTCGATTTAGAGAAGTAGTTGCTACGACATCTTCAAACAGACTGGTTGAACACG  
TTTGAGCAAGCGAATGGCACCAGGTTGCTCAAATTGAAAGATACCTTTTGTATTTCCAGA  
GGCAAATAAATCTAACGTTTCTTTGTCTTCCAAATCTATTTCTTCAATTTTAAGGTGAAT  
ACCTTCTGTTTCAGCAAGCAACTCTTGCATCTTCTGGACAAAGGTCAAATTTTCGTAGTCC  
CAGAAAGTCCATCTTCAAAGTCCGCTAGCCTCAACTCCATGAGCATCATACTGAGTCAG  
TGGAATTTTCATCACCATACTTTAGAGGAATGTAGTTGGTTAAATCTTGGTCACTAATTAC  
AACACCAGCCGCATGGACAGAGGTTTGCCCTTGATAGCCCTCTATCTTGCAAGCAATCTC  
AAAAGCTTTTTGGTATTCTAACTTACTATTGATTGGCTGACGAAACTGGAGATTGCCCT  
CATAGGCCGACTTAAGATTGTCACGAAAACCTGATTTTCTTAGTAATTGCAGATAATTTCAT  
ACTCTGGCACACCAAAGCGTTTCAAGACATCTCGAAGAGCTTGCTTGGCTCCAAAGGTTG  
AAAAAGTAACGATTTGTGCCGCATGTTTACTACCATATTTATTACCAACATATCTGATAA  
AATCTGGACGATAAATATCTGGGATATCAATATCAATATCAGGCATGGTATAGCGTTCAC  
GATTAAGAAAGCGTTCAAAAATCAGATTTTCTCTACTGGGTCAATCCCCGTGATGTCTA  
AGGCATAAGAAACCAAACCTGCCTACTGCAGAACCCCTTCCCATTCCCATATAATAGCCAT  
TCGATCGTCCAA

## ORF Predictions:

ORF #	Start	End	Direction	Length
6	295	2232	R	646 aa

[SEQ ID NO: ] 3864336-6 ORF translation from 295-2232,  
direction R

VCQSMNYLQLLRKS FVTILSRPMRAISSFVSQINSKLEYQKA FEIACKIEGYPRQTSVH  
AAGVVISDQDLTNYIPLKYGDEIPLTQYDAHGVEASGLLKMDFLGLRNLTFVQKMQELLA  
ETEGIH LKIEEIDLEDKETLDLFASGNTKGIFQFEQPGAIRLLKRVQPVCFEDVVATTSL  
NRPGASDYINN FVARKHGQEEVTVLDSALEDILAPTYGIMLYQE QVMQVAQRFAGFSLGK  
ADILRRAMGKKDASAMHEMRASF IQGSIEAGHTAEKSEQVFDVMEKFAGYGFNRSHAYAY  
SALAFQLAYFKTHYPAIFYQVMLNYSNSDYLIDALEAGFEVASLSINTIPYHDKIANKSI  
YIGLKS IGLSKDLALWII EHRPYSNIEDFIAKL PENY LKLPLLEPLVKVGLFDSFEKNR

QKVFNNLANLFEFVKELGSLFGDAIYSWQESDWTQEKFYMEQELLGIGVSIHXLQAIA  
SKAIYPITPIGNLSENSYAIILVEVQKIKVIRTKKGENMAFLQADDSKKKLDVTLFSDLY  
RQVGQEIKEGAFYYVKGIQSRDGRLOMIAQEIREAVAERFWIQVKNHESDQEISRILEQ  
FKGPIPVIIIRYEEEQKTIVSPHHFVAKSNELEEKLENEIVMKTIYR\*

Blastp and/or MPSearch Result:

Description:

DNA POLYMERASE III, ALPHA CHAIN (EC 2.7.7.7). - ESCHERICHIA  
COLI.

Assembly ID: 3864344

Assembly Length: 2244bp

[SEQ ID NO: ] 3864344 Strep Assembly -- Assembly  
id#3864344

GTTAACCTAGAGTAATCATTTTTTCAACAGTTTACGGATTCTTTAGCACGAGCTTCAG  
TTGTCACGATTGATTTCGTTGATCAAAAGGTCAGTTGTCAAATCGCGAAGCATTGCTTTAC  
GTTGTGAGCTAGTGCGTCCTAGTTTACGGTAAGCCATGTATTCCTCCTTTATTTATCTTT  
TAATCCAAGACCCAAATCAATGAGTTTGAGTTTCACTTCTTCCAAACTCTTGCGTCCAAG  
ATTTTCGTACTTTCATCATCTCTGCTTCAGATTTTTCTGTCAAATCATGCACAGTATTGAT  
ACCGGCACGTTTTAAACAGTTGTATGAACGCACAGACAAGTCCAGTTCCTCAATCGTACG  
ATCTAAAATACGGTCGTCAGATTCAGTATCAGCTTCTTTCATCACTTCAGTTGACTTAGC  
AATCTCAGTAAGATTTGTAAACAAATCAAGATGTTCTGTCAAAATACGTGCTGAAAGCCC  
TAAAGCATCTTCTGGAATAATTGTTCCATTTGTCAAGATTTCAAGGGTTAATTTGTGCGAA  
ACCATCATTGCTACCTACACGAGCAGGTTCCACTTGATAGTTGACTTTTGTAAGTGGTGT  
ATAAATAGAATCTACAGCAAGTGTTCCAAGTGGTGCATTATCCTTTTTATTTTCATCAGC  
AGGTACATATCCACGACCACTGTTAACAGTCATAGTCGCTTTTAGAGAAGAACCTTCACC  
AATTGTAAAGAGATAATGATCTGGATTTACAATTTCAATATCGCTATCTGTCAAAATGTC  
ACCAGCTGTTACTTCAGCAGGACCTTCAACATCCAGTTCGATGATTTTTTCGTCTTCAAC  
GTACGATTTCACTGCAATTCCTTTAATGTTCAAGATGATTTGCATCACGTCTTCACGAAC  
ACCTGGAAGTGTGTCAAACATCATGTAACACACCATCAATGTTGATAGATGTCACAGCTGC  
TCCTGGTAGAGAAGCTAGAAGTACACGACGAAGAGAGTTACCAAGAGTTGTACCGTAGCC  
ACGTTCAAGTGGTTCGATTACAACTTGCCATAATCTTTATTTTCATCAATTTTGTAT  
ATTTGGTTTTTCAAACTCGATCATTTAGTTACTCCCTCTTAAACGAAAAGCAGTGTAATG  
CGATGATTATACACGGCGACGTTTTTGAGGACGAGCACCATTGTGTGGCACTGGAGTCAC  
ATCACGAATTGCTGTTACTTCAAGACCAGCGGCAGCAAGCGCACGAATAGCTGACTCACG  
ACCAGAACCTGGACCTTTTACAGTAACTTCAACTGATTTAAGACCGTGTTCTTGTGCAGA

TTTAGCAGCAGCTTCAGAAGCCATTTGAGCAGCGAATGGTGTACATTTACGAGAACCTTT  
 GAAACCAAGAGCACCAGCTGATGACCAAGCAATTGCATTACCATGCACATCAGTAATCAT  
 AACAATAGTGTTATTAAATGTAGCGTGAATATGAGCAATACCAGATTCGATATTCTTTTT  
 CACACGACGTTTACGTGTTGGTTTAGCCAAGACTTTTACCTCCTATATTATTTTTCTTA  
 CCAGCAATCGCAACAGCTTTACCTTTACGAGTGCGGGCGTTGTTTTTAGTGTTTTGTCCA  
 CGGACAGGAAGTCCACGACGGTGACGGATACCACGGTATGAACCGATTTCATCAAACGT  
 TTGATGTTCAAGTTTACTTCACGACGAAGGTCACCTTCAACTTTGATTGCATCCACTTCA  
 CGACGGATAGCATCTTCTTGATCTGATGTAAGATCACGTACACGAACATCTTCTGAGATT  
 CCAGCAGCAGCCAAAATTTTCTTAGATGTTGCAAGTCCGATACCATAAACATAAGTCAAT  
 GAGATTACTACGCGTTTGTTCATTTGGAATATCAACTCCAGCAATACGAGCCATGTTTCCT  
 CCTTTCTATCTTATCCTTGACGTTGTTTGTGTTTTGGATTGCTGGGCAAATTACCATAA  
 CACGACCATTACGACGAATAACTTTACAGTATTCGCAAATTGGTTTGACCGATGGTCTTA  
 CTTTCATTTCTTATCCCTCCAAGTTTTTCGATTATTTAAAGCGGTAAGTGATACGTCCAC  
 GTGTCAAGTCATATGGACTCATTTTCGACAGTAACACGATCTCCCGCTAAAATACGAATAT  
 AGTTTTTACGAATTTTACCAGAACTGTTGCTAAAATCTGATGTTTCATTTTCAAGTTCCA  
 CCGTAAACATTGCATTCCGGCATT

## ORF Predictions:

ORF #	Start	End	Direction	Length
8	1147	1503	R	119 aa

[SEQ ID NO: ] 3864344-8 ORF translation from 1147-1503,  
 direction R

VKKNIESGIAHIHATFNNTIVMITDVHGNIAIWSSAGALGFKGSRKCTPFQAQMASEAAA  
 KSAQEHGLKSVEVTVKGPGSGRESAIRALAAAGLEVTAIRDVTPVPHNGARPPKRRRV\*

## Blastp and/or MPSearch Result:

## Description:

30S RIBOSOMAL PROTEIN S11 (BS11). - BACILLUS SUBTILIS.

Assembly ID: 3864352

Assembly Length: 2627bp

[SEQ ID NO: ] 3864352 Strep Assembly -- Assembly  
id#3864352

ATCGAATTATCTTGTATTTTCGTCTGCAAATGGCTAGATGGTAAGAAGTAGACCGACTGAC  
TAGCCTATAAACACCCGTTAAATCGCTAAGAAACGTCAAAAAAGCCCTTAACTATGGCAC  
TAGTTAGGGGCTTTGGTGTCTAATGAACCTTATACACTAACTACATTCTAGCATATAAG  
CCCAGATATTTCAAGAGTTTATTTATTTTTCAGGTTCCCTTAGTTCTGAAAGGTCTAT  
AATGAAGTTAGCCATCTAGTATCAAAAAACCGACTAGCTCTTATGAACTAGTCGATTTCT  
CATCAATGCGCCAACATTTCTTGAGCGATTTCTTGGCCAGATAGGTTATCTGGGTTAGTAG  
GTTGGCCAGTTGTCCATTTCTTCAAAGAGGGCTTCTTGGCTTGTGCCTCCAAAGAAGATA  
TGGAAATGTTCTGCCTTAACTGGGGCGATATTGTGGTCACTAACTGAACATACTTGAAT  
TGTCCAGCGTCAGCATCTGTGGCTTCAAAGAGGAAACGCACGCCACGATTGCCTTTCTTG  
TAAGTCAAAATTTTCTTACCGACATACTTGTAAGTGTATTTCTTGCTTTGTCCACCTTGA  
ACAAATTCCATAGTATTATCAGTAATGTTAATCTTAGTCACATCTGTCTGATAGCCTTTT  
GTATAGTAAGCCTTGTACTCAGCCTGGGTCATCTTACCAGTCAACTTAGCCTTGTAAGTCA  
AAGACTTGGTCAAACGTGCCGTCTTCAAAGGAAAGGATAAACTGATTGCCAGTTACCTGCA  
TAGTCACTCAAGGTGCGGTCTTGACAGCTGCATCCTCGAAGTAACCATTTTGGACTGTC  
TTGGTATCCTCTGCCTTTTTCAGGTTTCGATTGCTGGGCCTTCTTGGTCTGTTGTTTGTTC  
AAAGCCTTGAGGTTTTTCTCCATCACGGAAATGTAGTTTTCTCCAGCCTTGGTGTCTCT  
TCTGTGACACTTTCTAAAGGATTGAGGACATCAGTTTTTGACACCTGCTTCTTTTGAAAGT  
GTGTTAGCAAGGGCTTGTGAGGCATTTTCTTCAAATAGATATAAGCGATTTTATTTTTC  
TTGACATACTCTGTCAATTCTGCCAAGCGAGCAGCTGATGGCTCTGCATCTGGAGAAAGG  
CCTGAGATTGCGACTTGTTTGTGAGTCCATAGTCCAAGGCAAGATAGTTAAAGGCTGCGTGT  
TGAGTCACAAAGCTCTTTTGTTTGCTTGAGACAAGCCTTCTGCGTAAGCCTTATCCAAG  
GATTGCAATTTTTTCGATATAGGCAGCTGCATTCTTCTCAAAGGTCTCTTTTTTATCAGGA  
TAATCTGCTGACAAGCTGTGCGGATGTGCTCTACTAGTTTAAATGGCACGAACTGGTGAT  
AACCAAACATGGGGGTCAAACCTCATGGTGATGACCTTCTTCTCCATGGTCATGGTCTCCC  
TCTTCTTCTCGCCACCTGGCAAGAGCAACATATCGCCTGTGCGCTTGATGGTTTTCACT  
TTTTTCTTATCCAAGGTATCTAGCAATTTAGGTACCCATGTTTCCATGTTTTCATTTTTCA  
TAAACGAAGGTATCTGCATCTTGGATTTTGGCAACTGCCTTGGCAGATGGTTCGTATTCA  
TGAGGTTCTGTCCCAGCACCGATTAGGAGTTCTACATTAGCCGTATCTCCTGCGACTTGC  
TTGGTAAATTCATAGACAGGGTAAAAGGTTGTACGATATTGAGTTTACCATCTGCCTGT  
TTTTGATTGGAACAAGCCACTAAAAACAAGGCACATAGACTGGCTAGTAATAAGCTAATT  
TTTTTCACGTTTCGTCTCCTATTTGATAAAACGTCTTACTAACTGATTAGTATAAAGACA  
GTTACAAAAATAATGGTAATACTTGCCTTGCAGGTGTTTCTGCATAGTAGGAAATGTAA  
AGTCCTGCTACCATTCCCAAAAAGCCAATCGCACTGGCAAGCAGCATAACCGATTTAAAG  
TTTTTCCCCAGACGCAGGGCAATACTAGCTGGCAAGACCATAATGGTCGATACCAGAAGA  
GCTCCTGCTGCAGGAATCATAAGGGCAATAGCCACCCCTGTCACCATGTTAAAAAGAATG  
GACATGGTACGAACTGGCAAGCCATCCACAAAGGCCGTATCTTCGTCAAAAGTTAAGATA  
TACATAGGACGAAGAAAGAGAAAGGTCAAATCAAAACAACCGCCGCAATGACAAAAGAGG  
GAAATGACCTGTTCTTCACTGATAGTCACGATCGAACCAGAGATATTGGTCCAAACTC  
ATTGAACTCGAGTTTTTACCCTTGCTCATGACAATCAGAGAAACAGCCAGACCTGTTGAC  
ACGAGGATAGCTGTCCCGATTTCCATAAAGCTCTTGTAACCGTACGGAGATACTCCAGA  
AAGACCGCCGCAATCAAGACAATGGCAATAGTAGAAATAGTTGGAGAAATCCCCAAAACC



AGACCNAAGGATACACCTGAAAATGAGACGTGGCTAAGGGTATCANTCATCAAACCTCTGA  
 CGACGCACAGATGAGGAAGGTTCCCAATACCGNTGAGTAAAGACTCATAGCAATAACCGC  
 CAAAAGGCGCGTTGTATAAAGTCGTAAGATNATAAACTAAGCATGG

## ORF Predictions:

ORF #	Start	End	Direction	Length
6	303	1808	R	502 aa
7	1818	2528	R	237 aa

[SEQ ID NO: ] 3864352-6 ORF translation from 303-1808,  
 direction R

VKKISLLLLASLCALFLVACSNQKQADGKLNIVTTFYPVYEFTKQVAGDTANVELLIGAGT  
 EPHEYEPSAKAVAKIQDADTFVYENENMETWVPKLLDTLDKKKVKTIKATGDMLLLPGGE  
 EEEGDHDHGEEGHHHEFDPHVWLSPVRAIKLVEHIRDSLSADYPDKKETFEKNAAAYIEK  
 LQSLDKAYAEGLSQAKQKSFVTQHAAFNYLALDYGLKQVAISGLSPDAEPSAARLAELE  
 YVKKNKIAYIYFEENASQALANTLSKEAGVKTDVLNPLESLTEEDTKAGENYISVMEKNL  
 KALKQTTDQEGPAIEPEKAEDTKTVQNGYFEDA AVKDRTLSDYAGNWQSVYPFLEDGTFD  
 QVFDYKAKLTGKMTQAEYKAYYTKGYQTDVTKINITDNTMEFVQGGQSKKYTYKYVGKKI  
 LTYKKGNRGRVFLFEATDADAGQFKYVQFS DHNIAPVKAEHFHIFFGGTSQEALFEEMDN  
 WPTYYPDNLSGQEIAQEMLAH\*

Blastp and/or MPSearch Result:

## Description:

ADHESIN B PRECURSOR (SALIVA-BINDING PROTEIN). -  
 STREPTOCOCCUS SANGUIS.

[SEQ ID NO: ] 3864352-7 ORF translation from 1818-2528,  
 direction R

VRRQSLMXDTLSHVSFSGV SXGLVLGISPTISTIAIVLIAAVFLEYLRTVYKSFMEIGTA  
 ILVSTGLAVSLIVMSKGKNSSSMSLDQYLFSGSIVTISEEQVISL FVIAAVVLILTF LFLR  
 PMYILTFDEDTAFVDGLPVRTMSILFNMVTGVAIALMIPAAGALLVSTIMVLPASIALRL  
 GKNFKSVMLLASAIGFLGMVAGLYISYYAETPASASITII FVTVFILISLVRRFIK\*

Blastp and/or MPSearch Result:

Description:  
unknown

Assembly ID: 3864366  
Assembly Length: 1841bp

[SEQ ID NO: ] 3864366 Strep Assembly -- Assembly  
id#3864366

ATCGAATTCGAAC TAAGATAAAGGGGACATTGAAAGCATCAACTTGCAC TATGGGGACCC  
TTTTATCTTTATGGAGGAGTTTTATCAGGATACAAAAGAAATGGTCAAGATAACTTCTGG  
TACCTTATTTGACCATTTGGCAGGTTGAAGTGTCAGTTGACTTTGCACGTATCCAGTATCT  
CTTTGAGCTCAGAGATACAGAAGGTCAAATATTTTGTATGGCGATAAAGGGTGTGTGGA  
AAATTCTCTAGAAAATCTTCATGCAATCGGGAATGGATTTAAGTTGCCTTATCTTCATGA  
GATTGATGCCTGCAAGGTTCCCTGACTGGGTTTCAAATACGGTATGGTATCAGATATTTCC  
TGAAAGGTTTGCCAATGGCAATGCTCTATTAAACCCAGAAGGGACTTTAGACTGGGATTC  
ATCTGTACACCTAAGAGCGATGATTTCTTTGGTGGTGATTTACAGGGGATTATTGATCA  
TATGGATTACTTGCAAGACTTGGGTATTACTGGACTATATCTTTGTCCCATCTTTGAATC  
TACAAGCAATCACAAGTACAATACGACAGATTACTTTGAAATTGACCGTCATTTTGGAGA  
CAAGGAGACCTTTTCGGGAACTGGTGGATCAAGCGCATCATCGTGGCATGAAAGTCATGCT  
GGATGCGGTATTTAATCATATTGGTTTCGCAATCTCTTCAATGGAAAAATGTCGTCAAAAA  
TGGTGAACAGTCTGCTTATAAGGATTGGTTCCATATTCAACAATTCCCAGTGACAACTGA  
AAAGCTAGTTAATAAGAGAGACTTACCCTATCATGTTTTTTGGTTTTCGAGGACTATATGCC  
TAAGCTAAATACAGCCAATCCAGAGGTCAAGAATTATCTTTTAAAGGTTGCGACTTATTG  
GGATTGAAGAGTTTTAATATCGATGCTTGGCGTTTTGGATGTGGCTAATGAGATTGACCATC  
AGTTCCTGGAAGGATTTTCGTAAGGCAGTTTTAGCTAAAAATCCTGATCTTTATATCCTAG  
GAGAAGTCTGGCATAACATCTCAGCCTTGGCTAAATGGAGATGAGTTCCATGCCGTCATGA  
ATTATCCTTTATCTGATAGTATCAAGGACTATTTCTTACGAGGAATTAAGAAGACAGACC  
AGTTCATCGATGAAATCAATGGAGAGTTTATGTATTACAAGCAGCAGATTTTCAGAGGTCA  
TGTTTAATCTCTTGGATTACATGATACAGAGCGAATCCTGTGGACGGCCAATGAAGATG  
TTCAACTGGTTAAATCAGCCTTAGCCTTTCTCTTTTACAAAAAGGAACACCGTGCATTT  
ATTACGGAACCGAGCTAGCCTTGACTGGAGGACCAGATCCAGATTGTCGTCGTTGTATGC  
CTTGGGAACGTGTATCAAGTGACAATGATATGCTGAACTTTATGAAGAGGCTGATTAAAA  
TTCGGAATACGCGTCAGTAATCATTTTCGCATGGCAAGTATAGCCTTCAAGAAATCAAAT  
CTGATCTAGTAGCTCTGGAATGGAAATACGAAGGACGGATCCTCAAAGCAATATTCAACC  
AATCAACAGAAGATTATCTTTTAGAGAAAGAAGCAGTAGCACTAGCAAGCAATTGCCAAG  
AATTGGAGAATCAGCTTGTCATCTCTCCAGATGGATTTGTGATTTTCTAAAACTAGTTG  
ATGAAGATTATGGTACATTTTCATATCTTATATAGTATAATAAGGCTAGTTACTAACTTG  
TAAAGGAGAACTTAAATGAATTGTAGAGGACATGAAACAAGACAAAGAATTGTTAGAGAT  
TTTGAAGTTTAGCCTAAAGCACATATTAAGCTGTTAGCAA

## ORF Predictions:

ORF #	Start	End	Direction	Length
7	939	1670	F	244 aa

[SEQ ID NO: ] 3864366-7 ORF translation from 939-1670,  
direction F

VANEIDHQFWKDFRKAVLAKNPDLYLGEVWHTSQPWLNGDEFHAVMNYPLSDSIKDYFL  
RGIKKTDQFIDEINGEFMYKQQISEVMFNLLDSHDTERILWTANEDVQLVKSALAFLLFL  
QKGTPCIYYGTELALTGGPDPCRRCMPWERVSSDNDMLNFMKRLIKIRKYASVIISHGK  
YSLQEIKSDLVALEWKYEGRILKAIFNQSTEDYLLEKEAVALASNCQELENQLVISPDGF  
VIF\*

## Blastp and/or MPSearch Result:

## Description:

neopullulanase (EC 3.2.1.135) - Bacillus sp.

Assembly ID: 3864384

Assembly Length: 2026bp

[SEQ ID NO: ] 3864384 Strep Assembly -- Assembly  
id#3864384

CTGTTTAGCCTGGTTAAAGTCCTTGATGAATTTATTGACTTCGACGAATGTATTTCCAGA  
ACCAGCAGCAATACGACGGCGACGGCTTGGATTTAACAAATCTGGGTTTTACGTTCTTC  
AGATGTCATCGAAGACACAATGGCACGTTTACGAGCAATCTGGCGTTCATCCACCTTCAT  
GTTTTGAAGTGCTGGATTGTTGGCCATACCTGGAATCATCTTGAGCAAGTCTTCCATCGG  
CCCCATATTTTGCACCTGATCTAATTGATCGATGAAATCATTTAAATCAAAGGTGTTTTTC  
GCGCATCTTCTCAGCCATTTCAAGGGCTTTTTGTTTCATCGTATTCCTGAGAAGCTTTCTC  
AATCAAAGTGAGCATATCCCCCATGCCAAGGATACGGCTAGACATACGGTCTGGGTGGAA  
GGTTTCGATATCTGTAATTTTTTCACCTGTACCAGTGAAGTTGATTGGTTTTCCAGTGAT  
GTGACGAACAGACAGAGCAGCACCACCACGAGTATCACCATCAATCTTGGTAAGGATGAC  
CCCAGTCACTTCCAACTGAGCATTTAACTCACGCGCAACATTGGCTGCTTCCTGACCAAT  
CATAGCATCAACGACAAGCAAGATTTTCATTTGGTTGAGCCAATACTTTCACATCACGAAG

CTCATTCATGAGGAGCTCATCAATCTGCAAACGACCCGCAGTATCAATCAAGACATAGTC  
 GTTATGATTAGTTTGGGCTTGCTCCAAACCTTGACGTACAATCTCAACAGCTGGTACTTC  
 TGTTCGAAGTGCAAAGACAGGCACATCAATCTGTTGTCCCAAGGTCTTAAGCTGGTCAAT  
 GGCAGCTGGACGATAAATATCCGCCGCAATCATCAAAGGACGAGCATTTTCTTCTTTCTT  
 GAGTTTGTGGCCAAATTTACCAGCAAAGGTTGTTTTACCAGCCCCTTGTAACCAACCAT  
 CATGATGATGGTTGGAATCTTAGGTGACTTGATAATTCGATCTGCCGTATCAGAACCTAA  
 AACGGCTGTCAGTTCCTCATCAACGATTTTAATAATCTGTTGCGCAGGATTAAGTGTATC  
 AATGACCTCATGCCCCGACTGCACGCTCACGAACCTTTCTTGATAAAGTCCTTTACAACAGG  
 CAAGGCAACGTCGGCCTCGAGCAAGGCCAAGCGAATTTCTTTGGTTGCCTCTTGGACATC  
 AGATTCAGAGATTTTTCCTTTTTTACGTAGATTTTAAAGACGTTCTGCAAACGTTCTGT  
 TAAACTTTCAAATGCCATTTTTCTTCCTCTTATTCTCTATTATCAATGCTTGTTAAAATT  
 TCTATCTGCTCCTGCAGAAAATCATCCTTGGGATAGCGATCCAAGATTTGGTCAAAAATC  
 TGACTACGGACAATGTAGTCCGAGTACATGTGCAATTTTCATCTCATAATCTTCCAGAATC  
 TTTTCTGTTTCGCTTGATATTGTCATAGACAGCCTGACGACTAACACCAAACCTCCTCAGCT  
 ATCTCAGCAAGACTGTAATCATCAGCGTAGTAAAGCTCTATATAATTCATTTGCTTATCT  
 GTCAAAGCGCCCGCATAAAATTCAAAGAGCGGCCCATTCATACGATTGGTTTTTTCGA  
 TTTCCATAACTTTTATTATACCAAAAAATAGCCTAATCTACCACACTAGGGAGCCAATCC  
 TTGAAGATAGAAAGTAGATTTGAGAAAAACGAGATCCTAGCCCCAAGTAATTTCCAATTG  
 ATAGCTGGCAAAGGGATGCCCCCTCTTGATTTTGTTAGTTGATAAGCTAGCTCAATCTTTTG  
 CCTATCAACTTGATAACGGCTCGTTTGAATGATAAATTCCTGCATGCCCATAGGGGTAGG  
 AATATAGGCCAAACTATCACTATCCTTTAAAAAGCGCATAATGGTCTTGGGATTAGAAAA  
 TCGGCTCATCACCAGTTCTTGACCATGAAATTTAATAACTACTTTTTCTTTCTCATT  
 ATGAAAGAGTAAATAGCTATAATCTCCCTTTTCATGCACTTCCACA

## ORF Predictions:

ORF #	Start	End	Direction	Length
8	1717	2025	R	103 aa

[SEQ ID NO: ] 3864384-8 ORF translation from 1717-2025,  
 direction R  
 VEVHEKGDYSYLLFHNEEKEKVVIFHGGQELVMSRFSNPKTIMRFLKDSDSLAYIPTPMG  
 MQEFIIQTSRYQVDRQKIELAYQLQNQEGHPFASYQLEITWG\*

## Blastp and/or MPSearch Result:

Description:  
 unknown

Assembly ID: 3864400  
 Assembly Length: 1561bp

[SEQ ID NO: ] 3864400 Strep Assembly -- Assembly  
 id#3864400

CTTGATTATGGCTGTTTTGGAAAAACGGGCAGGGCTTCTCTTGCAAAATCAGGATGCCTA  
 TCTCAAATCTGCTGGTGGTGTAAATTGGATGAACCTGCCATTGACTTGGCTGTTGCAGT  
 TGCTATTGCTTCGAGCTACAAAGACAAGCCAATAATCCTCAGGAATGTTTTGTCGGAGA  
 ACTGGGCTTGACAGGAGAGATTCGGCGCGTGAATCGTATTGAGCAACGCATCAACGAAGC  
 TGCTAAACTGGGCTTTACTAAGATTTAAGTACCTAAGAATTCCTTGACAGGAATCACTCT  
 GCCTAAGGAAATTCAGGTCATTGGCGTGACAACGATTCAGGAAGTTTTGAAAAGGTCTT  
 TGCATAATCCGTGACAAATTCTCTTAAAAATGATAAGATAGGAGAAATATTTGACTATCA  
 AATTTTCAAGGAGGGAATCGTGTCGTATTTTGAACAGTTTATGCAAGCTAATCAGGCTTA  
 TGTGCCCCACATGGGCAGTTAAATCTGCCACTTAAACCCAAAACAAGAGTAGCTATTGT  
 GACCTGTATGGACTCTCGTCTGCACGTTGCGCAAGCTCTGGGCTTGGCACCTGGGGATGC  
 TCATATCTTGCGGAATGCAGGTGGTTCGAGTGACTGAAGACATGATTCGTTTCGCTAGTTAT  
 TTCCCAGCAACAAATGGGGACAAGAGAGATTGTGGTATTGCACCATACAGACTGTGGTGC  
 TCAGACCTTTGAAAATGAACCTTTTCAGGAGTATTTAAAAGAGGAATTAGGTGTAGATGT  
 GTCAGACCAGGACTTCTTGCCCTTCCAAGATATAGAAGAGAGTGTACGCGAGGATATGCA  
 ACTGCTTATCGAGTCTCCCCTAATACCAGACGATGTCATTATCTCTGGTGCTATTTACAA  
 TGTTGATACAGGAAGTATGACAGTCGTAGAATTATAAATACTTCATTTAGAAAGAAAGTG  
 TATGAAGAAAAGCAGTATTTTATTGCTATGTATTGGTTTACAGTATGAAACCATCTACTA  
 TACGGACGGTCCAAGGTCAGGTGCGGAATATGGACTAATGGGAGTTTCTATCTTTCTAGC  
 TCTCTTTTACATGATTCGGGCTCTTTATTTTCTCTTCCATATTGGGAAAAAATGGGAATT  
 GCCAAAGAAGGTTTTGATTCTGTCTTTATTGGGAGCAATCTGTTCCCTTACTTCTCTCTT  
 ACTATTTGGAATCTATAATCACAGACGAAAGTCATCTAAGGTATAAAAAATCGACCAGTT  
 ACTGGGGGTTCTTTTCCCAGATAGTACATTTTTAAATGCCTTTGAAAGTGCTATTGTGGC  
 TCCTTTGGTAGAAGAACCCTTGAAATTCGATTGCCACTTGTTTTTGTGTTTGGCTTTGATT  
 CCTGTGCGAAAATTAAAATCTTTGTTTTTACTTGGAATTGCTTCCGGTTTGGGATTCCAA  
 ATGATTGAGGATATTGGTTATATTCGTACGATTTGCCAGAGGGCTTTGACTTTACTATT  
 TCGCGAATTTTAGAGCGTATCATCTCAGGAATTGCCTCTCACTGGACTTTTTTCAGGTCTA  
 G

#### ORF Predictions:

ORF #	Start	End	Direction	Length
7	371	937	F	189 aa

[SEQ ID NO: ] 3864400-7 ORF translation from 371-937,  
direction F  
VTNSLKNNDKIGEIFYQIFKEGIVSYFEQFMQANQAYVALHGQLNLPLKPKTRVAIVTCM  
DSRLHVAQALGLALGDAHILRNAGGRVTEDMIRSLVISQQQMGTREIVVLHHTDCGAQTF  
ENEPFQEYLKEELGVDVSDQDFLPFQDIEESVREDMQLLIESPLIPDDVIISGAIYNVDT  
GSMTVVVEL\*

Blastp and/or MPSearch Result:

Description:  
unknown

Assembly ID: 3864416  
Assembly Length: 2009bp

[SEQ ID NO: ] 3864416 Strep Assembly -- Assembly  
id#3864416  
AATGATTTTCAAGCAGACGATCCATGTCATTTCAAGGAATACATGCGACGATTTCCCTTC  
GTTTCGATCGGGCTTGATCAACTCTTGATCTTCATAATAACGAATCTGACGCGCCGATAG  
ATCGGTCAACTTCATAACACTGCCGATAGGAAAAACAGCCATATTTCTGGCGAAATTCTTT  
TTCCTTCATTTACAATTTCTTCTTTCTGTCTATTATAGTCTAAAAAAGACAAACGTCA  
ATTGATAATGTTATAAAATGTAACATTATTTTTCTTTATTCTCTAAAAAGAGACGAATAC  
GATCAATATCGTAATTTACGATAATTGCGACAAAAACTCCCATAAACGTTTCTAAAAACAC  
GCACAAACACGTACAAAATTGTCTCACCCTTGGAATTGATAGGGTAATGATTAACATAG  
CTGCTACACCACCAATAACCCCTGCTTTGTTATTCATGGCTACATTTGTCTATAATGGTTA  
ACATGGTGCAGATTGGAACAACCTACCAAGGTCACCCAAAAGGCTTCGTGGAAAAAGGTAT  
TTAATAAGAAGAAGACCAAGGCATAGAGTCCACCGATACTATTTCTTAGAATACGCGAAG  
TCCCCAAAATGAACACTCTCATCAAACTCTCCCTCAGGCTAAAAACGGCTGTCAAAGCAC  
CAATTTGAAGACCTTTCCAGCCAAAAAAGCCAAAAATCAAGAGAACTAGAAAAACAGCAA  
TACCTGTTTTAAAGGTTTCGCATACCAAGTTTGAACCTGGGATTTATCGAATTTATATTTTT  
TAAAATAACTCATAATCTCAACTTTCTATTTCCATTTTATCATAAATCGGTGATTTTTAT  
GAGTAATAGTTGAGAGGAAGCGTTTTTTATTTTAAGCAAAAGAAAAGAGGAACCTTTCATCC  
CTCTCTTCTTTGATTTATTTATAAAATCTTATTTTTCTGTCAAGGCTGCAAGTCCTGGAA  
GAACCTTACCTTCAAGAAGTTCCATTGATGCTCCACCACCCGTAATAATCCATGAGAACT  
TGTCTGCACGGCCAAGGTTAATCGCTGCGGCAGCTGAGTCACCACCACCGATGATTGATT  
TAACTCCTGGTTGTTTCACGATAGCGTCCATCACACCGATTGTACCAGCTCTGGAAATCT

GGGTTTTCAAATACACCCATAGGTCCGTTCCATACAACTGTTTTAGCACCAGTCAAAGCT  
 TCGTCAAATTTGGCGATAGATTTTGGACCGATGTCAAGACCAAGGAAGCCTTCAGAAACT  
 GCTTCACCTTCAGTGTCAACGCACCTTCAGTGTAAACCAGCAAATGCGTTAGCTTCTTTTGA  
 GTCAACTGGCAAGATCAATTTACCATTTGCTTTTTCAAGAAGAGCTTTCGCAACATCCAG  
 TTTGTCTTCTTCTACAAGTGAGTTACCGATTTTCGATACCTTGTGCTTTGTAGAATGTGTA  
 AGTCATCCCACCACCGATAAGGACTTTATCAGCTTTTTCAAGCAAGTTTTCGATAACACC  
 GATCTTGTCTGAAACTTTTGAACCACCAAGGATAGCCACAAATGGACGTTCTGGAGTTTC  
 AACTGCTTCTTGGATGTAGGCAATTTTCGTTTTTCAAGAAGGAAACCAGCAACTGCTTTTTTC  
 AACGTTTGCTGAGATACCAACGTTAGATGCGTGTGCACGGTGAGCTGTACCGAATGCATC  
 GTTTACGAAGATACCATCTCCAAGTGATGCCAGTATTTACCAAGTTCAGGATCGTTTTT  
 AGATTCTTTCTTGCCGTCAACATCTTCGTAACGAGTGTTTTCAACCAAGAGAACTTGTCC  
 ATCTTCAAGAGCGTTGATTGCCGCTTCCAATTCAGCACCACGAGTGACACCTGGGAAAAC  
 AACATCTTGACCAAGTTTTGCTGCCAAGTCAGCTGCTACAGGAGCAAGTGATTTACCAGC  
 TTTATCAGCTTCTTCTTTCACACGTCCAAGGTGAGAGAAAAGAATTCGATGTCCACCTTG  
 TTCGATGATGTACTTAATAGTTGGAAGAG

## ORF Predictions:

ORF #	Start	End	Direction	Length
7	929	1189	R	87 aa

[SEQ ID NO: ] 3864416-7 ORF translation from 929-1189,  
 direction R  
 VLKQLYGTDLWVYLKTQISRAGTIGVMDAIVKQPGVKSIIGGDSAAAAINLGRADKFSW  
 ISTGGGASMELLEKGKVLPLAALTEK\*

## Blastp and/or MPSearch Result:

## Description:

PHOSPHOGLYCERATE KINASE (EC 2.7.2.3). - YARROWIA LIPOLYTICA  
 (CANDIDA LIPOLYTICA ).

Assembly ID: 3864424  
 Assembly Length: 2299bp

[SEQ ID NO:     ]     3864424 Strep Assembly -- Assembly  
id#3864424  
TGTGAAAGAGTCCATGGTTCCGATGGCAGCGTTGGGTAGGTCTGCCAACTGGCGACCCAA  
GTGTTGTTTTGAGCTCGACATCATCTGTTTTCTTGATTCTTGCTGATTTTTTTCTCTA  
AACGTTCTTTAAGTTCAGTTGCAGCCTTGACGGTAAAGGTTGAGATAAAGAGTTGAGAAA  
TTTCGACACCACGCGCCAATTGGTCCAGAATGCGCTCTGCCATGACAAAGGTCTTTCCAG  
AACCAGCCGATGCTGAGACCAGGATATTCTGGCCAGAAGTGTAGATAGCTTCGATTTGCT  
CGGCAGTTTTCTTCTGTTCCCTTGCTCGAATTTGCTTCTGCTTCTTGCAAGTTTTGAATCT  
CCTCCTCACTTAAAAAGGGAATAAGCTTCATCGATTCAACTCCTCTCTAATTTTTTCAAC  
CCAAGCTTGCTTGAGTTTTTCTCCGACCAGACGCTTGCTATCAGCTAGGTCCAACTTTTT  
TAGGAAACGGGCTTGGCCAGATGGTAATTGGCTTCAAAGCCTGTAATAGCCTGATGTTG  
CTGGACGTATGGGGCAATGCTTCTGCCATTTTCAGTATAAGGATTGATGGCGAACC GGCC  
TGCTAAAATCTTCTCAGCAGCTTTCTTGTAAGATAGGCATTGTAGTCCAGTAGGAGCTG  
AAATTCCCTCATCTGTCAGTTGATTAGCCTTGTTTTGTATATAAAATTCGCCTAAATAACT  
GCTTCTTTTTTCCAAGAAGAGCCCTTGGTATTTTCATAGATTGCTGGCTTCTACCACTGC  
TCCTGCAAGACTTTTTACCGCCATCAGAGATTGGACAGGTTCAAGCATTTCGAAGTACAT  
GGCGCCGAAAAGTTCTGCTCCCTTCTCTTTTTTAGGGCAGCAAGATAGGTTGGTAACTG  
AGAATTGAGCCCATTAAGAAATGAGGAACTGGAAGTGAAGTCAGACTGGATTGTAGTC  
TACTACTCCTATCGCTCCATTAGCTTTCAAACGGTCAATCCGGTCCACCTTGCCCTCGTAC  
AAAGACACTGCGTCCATTGTCTAATTGAATAAAGGCTTGGTCTTTTCCACCAAAAATTTGC  
TTCTTCTTTGATGGTTTCGATGGCTGGATTGTGTGCGAGAATATGTCCAGTCGTCCGTGC  
AACATCAAGCAAACTTCCTTGGTAACTGGGCTTCCAACTTTCTTGATAAATAGCTTC  
AAATTGCGTTCCTTGACTGGTTCTTGAATAGCTTGTTCTAGACGTTGGTCAAAGGAATC  
TTCATTAGGCAACTGTAAGGCGCGTTCAAAGATACGATGCAAGAAATTCCTGCTGACTACG  
GGCATCAGGATGCAAACGAATTCCTCCTGCAAGCCTAAAACGTAGCGTAGGAAATAACTG  
TATTCATTGCGATAAACTCTGTCAAACCCGACGTAGACAGGTAAAACTCCTGTTTGGCA  
GGATAGAGAGCTTGCAAGGTGTCCTTGGCTAAGGTCTTGCTGCTTGGACTGATTGGGATG  
GCTGGATTTTCCAGACCTTGCTGATCTAGTTTTTTTACCTATGACACGCGACAGAACCTTG  
ACAAAAGTCAAATCTTGCTCAGTATCGCTCATCTCACCCTGCTGGTGATAGGCAACCAGA  
CTAGACAAAAGACTGTGATAGGACCCCATATCCTCCTTAGACAGTCCTTTGTGATTCATC  
CTCTTCTCTCTCCGCCTAAATCCAAAATGGATCAACTCTTGAAGATAGGCAGATTCCTTA  
CTTTCACTTTCGTTAAAAAGGCTTGGAGCCGACAAGAACAACCTGCTTACGAGCAGAAATG  
ACCAAGGAAAGCATAGTGTAGCGATTTTTCTTGAGATTTTCACTGCTGGCAATCAGTAAT  
TGAACGCCTTCTTCGGTCGCTTGGTTTTAGGTTTTGCCTTTCTTCATCTGTCAGAAGACTG  
GTGTTTTGAGAAATTTTTGGTAAATTCGATCCTGAGTTAGTCCAATAGCATAGACAAAGT  
CAGCAGTCAATGGTGCAATCAAATCGTAACTCTGCACCAGAACAGTGTCCACTGTTGCTG  
GAATGGTACGGTATTGGGACAAACTCATTCCAGAATGGAGCAAGGCTAGGAAGTCTTCCA  
GACTAACCTGTGAACCAGCAAAAACAGTCGCAAAATGTTCTAAAACATGGCAGAAAGCCT  
TCCAAACTTCGGCTTGTCTTTTCTGTTCTACAGCTTCCAAAGTGGTTGTCAAATCTTGTA  
ACTGCTTGGTCACAGCTCCTTCTTTTAGAAAGACACTCCATTTTTGTAGGAGTTTTTCAA  
CCTTTTGTTCCTCGCTGGC



## ORF Predictions:

ORF #	Start	End	Direction	Length
7	388	1008	R	207 aa

[SEQ ID NO: ] 3864424-7 ORF translation from 388-1008,  
direction R

VDRIDRLKANGAIGVVDYKSSLTQFQFPHFNGLNSQLPTYLAALKREGEQNFFGAMYLE  
MAEPVQSLMAVKSLAGAVVEASKSMKYQGLFLEKESSYLGEFYNNKANKANQLTDEEFQLLL  
DYNAYLYKKAAEKILAGRFAINPYTENGSRISIAPYVQQHQAITGFEANYHLGQARFLKKLD  
LADSKRLVGEKLLKQAWVEKIREELNR\*

## Blastp and/or MPSearch Result:

## Description:

unknown

Assembly ID: 3864430

Assembly Length: 1915bp

[SEQ ID NO: ] 3864430 Strep Assembly -- Assembly  
id#3864430

AGAGGTAGGTCGTAAACGTAAAAAATTCTAATTGAAATGAAAGGGCTAGAGGAAATCTAG  
TCCTTTTTCTTTTAAATAAATACTCCAAAGCCTGCAAAAATCTGAAACTTCCTCCTACAA  
TTTGATATAATAGAGAGAAGAATTCATTTGAAGGAGGAAATGATGTCGGTTTTAGTAAAA  
GAAGTGATTGAAAAGCTTAGACTAGATATTGTCTATGGTGAACCAGAATTGCTTGAAAAG  
GAAATCAATACAGCGGATATTACGCGACCTGGTCTTGAAATGACAGGCTATTTTGACTAC  
TATACACCAGAGCGGATTCAACTTTTGGGGATGAAGGAGTGGTCTTATCTGATCAGCATG  
CCTTCCAACAGCCGTTATGAAGTTTTGAAAAAATGTTTCTACCTGAGACACCAGCAGTC  
ATTGTTGCCCCGTGGTTTGGTGGTTCAGAGGAGATGTTAAAGGCTGCTAGAGAATGTAAG  
ATTGCTATTTTAACCAGCCGTGCAGCTACCAGTCGTTTATCTGGAGAGTTATCTAGCTAT  
CTGGATTCTCGTTTGGCAGAACGTACCAGTGTGCACGGTGTCTTGATGGATATTTATGGG  
ATGGGCGTCTTGATTTCAAGGAGATAGTGGGAATTGGTAAGAGCGAGACAGGTCTTGAGC  
TTGTCAAACGTGGTCACCGTTTGGTAGCCGATGACCGTGTGCGATATCTTTGCCAAGGATG  
AGATTACTCTCTGGGGTGAACCAGCTGAAATTTTGAAACACTTGATTGAAATTCGTGGGG  
TTGGTATTATCGATGTTATGAGTCTCTACGGTGCGAGTGCTGTCAAGGATTCTTCACAGG

TTCAGCTTGCTGTCTATTTGGAAAATTACGATACGCATAAGACCTTTGATCGTCTTGGAA  
 ACAATGCAGAGGAACCTGAAGTTTCTGGCGTAGCCATTCCCTCGTATTTCGTATTCCAGTTA  
 AACAGGTCGTAATATCTCTGTTGTGATTGAGGCAGCTGCCATGAATTATCGTGCCAAGG  
 AAATGGGCTTTGATGCTACCCGTTTGTTCGACGAACGACTGACAAGTCTCATAGCTCGAA  
 ATGAGGTGCAAAATGCTTGATCCAATTGCTATTCAACTAGGACCCCTAGCCATTTCGTTGG  
 TATGCCTTATGTATTGTGACAGGCTTGATTCTTGCGGTTTATTTGACCATGAAAGAAGCA  
 CCTAGAAAGAAGATCATACCAGACGATATTTTAGATTTTATCTTAGTAGCCTTTCCCTTG  
 GCTATTTTAGGAGCTCGTCTCTACTATGTTATTTTCCGATTGATTACTATAGTCAGAAT  
 TTAGGAGAGATTTTGGCCATTGGAATGGTGGTTTGGCCATTTACGGTGGTTTGATAACT  
 GGGGCTCTTGTGCTCTATATCTTTGCTGACCGTAAACTCATCAATACTTGGGATTTTCTA  
 GATATTGCGGCGCCTAGCGTTATGATTGCTCAAAGTTTGGGGCGTTGGGGTAATTTCTTT  
 AACCAAGAAGCTTATGGTGCAACAGTGGATAATCTGGATTATCTACCTGGCTTTATCCGT  
 GACCAGATGTATATTGAGGGGAGCTACCGTCAACCGACTTTCCTTTATGAGTCTCTATGG  
 AATCTGCTTGGCTTTGCCTTGATTCTGATTTTGTAGACGGAATGGAAGAGTCTCAGACGA  
 GGTTCATATCACGGCCTTTTACTTGATTGTTGGTATGGTTTTCGGTCGTATGGTCATCGAAGGT  
 ATGCGAACAGATAGTCTCATGTTCTTCGGCCTTCGAGTGTCCCAATGGCTGTCAGTTGTC  
 TTTATCGGTCTCGGTATAATGATCGTTATTTATCAAAATCGAAAGAAGGCCCTTACTAT  
 ATTACAGAGGAGGAAAATAAATGTTAGAAGTTGCATATATCTTGTGTCCTAG

## ORF Predictions:

ORF #	Start	End	Direction	Length
7	627	1100	F	158 aa

[SEQ ID NO: ] 3864430-7 ORF translation from 627-1100,  
 direction F  
 VGIGKSETGLELVKRGHRLVADDRVDIFAKDEITLWGEPAEILKHLIEIRGVGIIDVMSL  
 YGASAVKDSSQVQLAVYLENYDTHKTFDRLGNNAEELEVSGVAIPRIRIPVKTGRNISVV  
 IEAAAMNYRAKEMGFDAIRLFDERLTS LIARNEVQNA\*

## Blastp and/or MPSearch Result:

Description:  
 unknown

Assembly ID: 3864442

Assembly Length: 2245bp

[SEQ ID NO:       ]     3864442 Strep Assembly -- Assembly  
id#3864442  
ATCGAATTTGAAGTGGTTTGAAGAGAGTACAACCTTGTCTTTTAGAAAAGGAGCCTATAAT  
GAAAGTCTTTTCAGCATGTAAATATCGTGACTTGTGATCAAGATTTCCATGTTTATCTTGA  
TGGAATCTTAGCAGTCAAGGATTCTCAAATCGTCTATGTCGGTCAAGATAAGCCANCGTT  
TTTAGAACAAAGCTGAGCAGATTATAGACTATCAGGGAGCTTGGATTATGCCTGGTTTGGT  
CAATTGTCAACCCATTCTGCAATGACAGGTCTGAGAGGGATCCGAGATGACAGCAATCT  
CCATGAATGGCTCAATGACTATATCTGGCCAGCAGAATCTGAGTTTACTCCCGACATGAC  
TACCAATGCGGTCAAAGAAGCCCTAACAGAGATGCTCCAGTCAGGAACAACAACCTTTAA  
CGATATGTATAATCCCAATGGTGTGGATATCCAGCAAATTTATCAGGTGGTGAAAACCTC  
CAAGATGCGTTGTTATTTTCTCCGACTCTCTTTTCTTCAGAGACAGAAACAACCTGCTGA  
GACTATAAGCAGAACTCGATCCATCATAGACGAAATCTTAAATATAAAAATCCAAATTT  
CAAGGTTATGGTAGCACCTCATCTCCGTATAGCTGCAGTAGAGACTTGCTGGAAGCGAG  
TTTGGAATGGCAAAGAGCTAAATATTCCGCTCCATGTCCATGTGGCGGAGACCAAGGA  
AGAGTCAGGAATTATCCTCAAACGGTACGGCAAACGCCCCCTTGCTTTTCTGGAAGAACT  
GGGTTATTTAAGATCATCCGTCCGTATTTGCTTCACGGGGTCAATTAAACGAGAGAGAA  
ATTGAACTTCTTGGCATCTTCTCAAGTGGCTATCGCCACAATCCTATCAGTAACCTCA  
AACTGGCATCAGGAATTGCTCCAATTATCCAGCTCCAAAAAGCGGGAGTAGTAGTCGGAA  
TTGCGACTGACTCGGTTGCTTCCAATAACAATCTAGATATGTTTGAGGAAGGAAGGACTG  
CAGCTCTTCTTCAGAAGATGAAAAGTGGGGATGCCAGCCAGTTTCCAATCGAAACAGCTC  
TCAAGGTACTGACAATCGAAGGGGCTAAGGTCCTTGGAATGGAAAATCAGATAGGAAGTC  
TGGAAGTCGGCAAGCAAGCAGATTTTCTGGTCATTCAACCACAAGGGAAAATTCATCTCC  
AACCTCAGGAAAATATGCTGTCTCACCTGGTATTATGCACTTAAATCTAGTGATGTAGATG  
ATGTTTATATCGCCGGAGAACAGGTTGTTAAGCAAGGTCAAGTCCTGACAGTAGAACTTT  
AAAAGAAAAATCACGAAAAATTTTAAAAAAAGTTCTGCAACAAATCTTGCATTCTTTTTT  
TGACTATGCTATACTTATATACGGTTTAAAAAACTGCCTAAGACAGTAGGGGAGCTCGA  
CTCATAAATATCCTACCGAGGACAAAACGTATCATGTAAAAAGAAGCGTATTGTACTTTC  
GTGTCTAGGTTTGGGCGCGTTTTTCTTTTTGAAAAATTCCCAAGCAAATAATTACGGA  
GGTGAACACACTAATGAGTGAAGCAATTATTGCTAAAAAAGCGGAACTAGTTGACGTAGT  
AGCTGAAAAAATGAAAGCTGCTGCATCTATCGTCGTTGTAGACGCTCGTGGTTGACAGT  
TGAGCAAGATACAGTTCTTCGTCGTGAGCTTCGTGGAAGCGAAGTTGAGTATAAAGTTAT  
TAAAACTCAATCTTGCGTCGTGCAGCTGAAAAAGCTGGTCTTGAAGATCTTGCATCTGT  
ATTTGTTGGACCATCTGCAGTAGCATTTTCTAATGAAGATGTTATCGCACCAGCGAAAAT  
CTTGAACGACTTTTCTAAAAACGCTGAAGCACTTGAAATTAAAGGTGGTGCAATCGAAGG  
CGCTGTCGCATCTAAAGAAGAGATTCTTGCACTTGCAACTCTTCCAAACCGCGAAGGACT  
TCTTTCTATGCTCCTTTCTGTACTTCAAGCGCCAGTGCGCAACGTTGCTCTTGCAGTCAA  
AGCGGTTGCAGAAAGCAAAGAAGACGCGGCTTAATCTTAAGCTACACAGCGTAGCCTAGC  
TACGAAAAAACTATTATAAAATTTAAACTTATTTGGAGGAAATAACAATGGCATTGAA  
CATTGAAAACATTATTGCTGAAATTAAAGAAGCTTCAATCCTTGAATTGAACGACCTTGT  
AAAAGCTATCGAAGAAGAATTCGAT

## ORF Predictions:

ORF #	Start	End	Direction	Length
7	867	1322	F	152 aa
8	1562	2074	F	171 aa

[SEQ ID NO: ] 3864442-7 ORF translation from 867-1322,  
direction F

VAIAHNPISNLKLASGIAPIIQLQKAGVVVGIIATDSVASNNNLDMFEEGRTAALLQKMKS  
GDASQFPIETALKVLTIEGAKVLGMENQIGSLEVVGKQADFLVIQPQGKIHLQPQENMLSH  
LVYALKSSDVDDVYIAGEQVVKQGQVLTVEL\*

Blastp and/or MPSearch Result:

## Description:

N-ethylammeline chlorohydrolase [Rhodococcus corallinus]

[SEQ ID NO: ] 3864442-8 ORF translation from 1562-2074,  
direction F

VNTLMSEAIIAKKAELVDVVAEKMKAASIVVVDARGLTVEQDTVLRRELRGSEVEYKVI  
KNSILRRAAEKAGLEDLASVFGPSAVAFSNEDVIAPAKILNDFSKNAAEAIKGGGAI  
EG AVASKEEILALATLPNREGLLSMLLSVLQAPVRNVALAVKAVAESKEDAA\*

Blastp and/or MPSearch Result:

## Description:

50S RIBOSOMAL PROTEIN L10 (BL5). - BACILLUS SUBTILIS.  
(BLAST)

Assembly ID: 3864450

Assembly Length: 1471bp

[SEQ ID NO:     ]     3864450 Strep Assembly -- Assembly  
id#3864450

GGGAGAGAACTGTGACAGAAAAACCAACAAATACTCGTTCTCTAACTGCAGAAGATTTGG  
TGAAGATTTCCAAAGGGGAATTGCATTTAGAAAATGATTTGATTGATGAATCTTTCTATG  
GTGAAAAAGCTCTTGATTTGGAAGGGGATGATTACCAGGATGGCATCAAAAACAAAGATG  
GTAAGGATTATCTAGGATATAACAGTCATCCCTTGCTAGCAGACAGTGATGGGGATGGTT  
TGGCAGATGGGGAAGATGATAATAAGAAAGAATGGTATGTCACAGACCGTGATTTCTCTTC  
TCTTTATGGAGTTAGCTTATCGAGACGATGATTATATTGAGAAAATTTTAGATCATAAGA  
ATCTTTTCCCTAGTCTCTATCTTGACCGTCAAGAACACAACTCATGCACAATGAATTGG  
CTCCTTTCTGGAAGATGAAAAAGCCTACTATACAGATAGTGGCTTGGATGCTTTCTTAT  
TTGAGACCAAGAGCGACCTTCCTTATCTCAAAGATGGAACGGTGCACATGTTGGCTATTC  
GTGGAACGCGAGTTAATGACGCCAAGGACTTGAGTGCAGATTTTGTGTTTATTAGGTGGAA  
ATAAACTAGCTCAAGCGGATGATATCCGCAAGGTTGTTGGGGAATTAGCCAAGGATATAA  
GTATTACTAAGTTGTATATGACAGGTCATTTCTCTTGGAGGCTACCTAGCTCAGATTGCAG  
CGGTTGAAGATTACCAAAAATATCCTGATTTTTTATAACCATGTATTGAGGAAAGTGACAA  
CTTTCAGTGCTCCTAAAGTCATTACTTCCAGAACTGTTTGGGATGCTAAGAATGGTTTCT  
GAGATGTTGGTTTGGAAAGTCGTAAATTAGCTGTTAGTGGAAAAATTAAGCATTATGTGG  
TTGATAATGACAATGTTGTGACTCCCTTGATTCATAATAATCGTGATATTGTTACATTTA  
CAGGTAATTCACGCTTTAAACACCGTTCTCGTGGCTATTTTGAAAGTCCAATGAATGATA  
TTCCTAACTTTAATATTGGTAAACAAGCTACCTTGGATAAACATGGTTATCGTGATCCGA  
AATTGGATAAAGTGCGATTCTTTAAGAAACAGGCTCTACCTCAATCTTCTAGTCAACCAA  
GCGCTGAACCAATGGAAAATATTGCCTTAGGAAAACAGGTTACTCAAAGTTGACAGCTT  
TCGGAGGAGATGCTAGAAGAGCTGTGGATGGCAAAGTCGATGGTAACTATGGTCACAATT  
CTGTCACTCATACAAACCTCCAATCTAAGCCTTGGTGGCAAGTAGATTTGGCTAAAGAAG  
AAACCATTCGCCAAATCAATATTTACAACCGAACAGACACTGCCCAGGATAGATTGGCAA  
ACTTTGATGTCATTCTTTTAGACAGTTCTGGTAAAGAAATTCGAGTGAAAACGTATAATA  
TCTCCTAAAGATGTGTCAGCACAAATTCGAT

## ORF Predictions:

ORF #	Start	End	Direction	Length
7	897	1448	F	184 aa

[SEQ ID NO:     ]     3864450-7 ORF translation from 897-1448,  
direction F

VVDNDNVVTPLIHNNRDIIVTFTGNSRFBKHSRGYFESPMNDIPNFIKQATLDKHGYRD  
PKLDKVRFFKKQALPQSSSQPSAEPMENIALGKQVTQSSTAFGGDARRAVDGKVDGNYGH  
NSVTHTNFQSKPWWQVDLAKEETIRQINIYNRTDTAQDRLANFDVILLDSSGKEIRVKTY  
NIS\*

Blastp and/or MPSearch Result:

Description:

unknown

Assembly ID: 3864482

Assembly Length: 1954bp

[SEQ ID NO: ] 3864482 Strep Assembly -- Assembly  
id#3864482

CTACGATAAAGTCACCAGAGTCATTAGCAGGTGCTTGAACAAGTTCCTCAGTTTTTTCTG  
AAGCTTGGTCAAAAAGTTCGATAACTTGGTCTGCAGATGTTGCTTGACGAAGTTTGTCTG  
CAAAACCGTCTTTTCATCAAGTATTGAGACAATTCTGTCAATGCTGCCAAGTGAGTATCAT  
TGGCACCTTCTGGAGCTGCAATCATGAAGAAGAGGTCAGTTGCCTGCCCATCCAAACTCT  
CATAGTCAACACCCTTGTTTTGACTTAGCAAAGAGAACTGTCGCTTCTTTGACAGCAGCGT  
TTTTGCTGTGAGGCATAGCGATTCCATCACCCAAACCAGTAGAAGTTAAAGCTTCACGCG  
CCAAAATGCCTTCTTTAAAGGTTTCAAAATCTGTACATAACCGTGGCCTGTTAGGCTTT  
TAATCATCTCTTCAATGACAGCAGTCTTTTCAGTTGCCTGCAAATCCAGCAACATGACAT  
CTTTTCTCAATAAATCTTGAATTTTCATCGTTTTTTCTACCTCAACTTTTCCATATGTTTC  
TTTAATAAATTCGCGCGTTGCCAAGTCATCTGAGAAGGTAGTTGCCGTTCCGCAAGCCAC  
TCCCCATTTGAAGGCTTCTACTGCGTCTTTTGATTTGACAAATTCACCTGTGAATCCAGC  
AACCATAGAATCACCAGCTCCAACGAATTTTGTACTGTTTCCTTTGATTGGTTTAGCGAA  
GTAAGCTCCCTCAGATGTGACAAGAAGGGCACCATCACCAGCCATAGAGATAATAACATT  
TTGAGCACCCCTTAGCCAGTAACTCACGAGCGTATTTCTCAATTTTCATCTAAACTTTTCGAG  
TTTAACCCCAAAAATCGCTCCAAGTTCATGATTATTTGGTTTTACAAGAAGAGGCTGGTA  
ATCCAAACTATCAATTAAGGTCTGTCCTTCAAAGTCACAGACCACTTGCGCACCAGTCTG  
GCGCGTCAAGGAAATCAAATCCTTATAGATAACATTGCCTAGATTTTTTAGCACTTGAACC  
TGCAAAGACAACGTGTATCTTCTGCTGTCAGACTAGATAAAATAGCTTTCAATTCTTCTAG  
CTTAACCGGTTCAACAGTTGGACCCGTTCCGTTGATTTCTGTTTCTTGGTCTGCTTNGAT  
TTTAACATTGATACGAGTATCTTCTGCCACCTGGACAAAAGGGTCTCGATTTCTTCCTC  
TGGCTAAAGTATCTGTGATAAATTTACCAGTAAAGCCACCGATAAATCCCGTTTCGCTGTA  
TTTGATATATTCAAACGTTTCAAGACACGGCTGACATTGATTCCTTTCCCACCAGCAAAC  
TTATCATCACTGTCCATACGATTTACACTACCAACTTTGACTTGGTCCAAACGAACGATA  
TAGTCAATGGATGGATTGAGTGTGACTGTATAAATCATACTTCTATTACCTCCGTTTTCT  
CCTTAATAACCTGCAAGAGCTCATGCCCTTGACTAGTGATAACGATAGCGCGTTTGAGTG  
GGGCTACCTTGGAAGCAAGTTTGTCCAATTTTTTGACGAATCCACCAAGACGTAGGTCT  
GCTTGGCATTTCCAAAATAGCTCTTTTTCACAGCTCCCTCCTCCATATCAGGAGTCGTAT  
AATAGCCATCGTCAACACCATTTCATTCCGATAAAGGCACGGTCAAAGTGCAATTGGTTAA

TCTGGTTAAGAGCAACGCCCCGATACTAGCATCTGTCGCCGTCTTGACGTTTCCTCCAA  
 CCATGACAGTTGGAATCTGCTTTTCAACCAACTGAGCGGCATGGTGAATGGAGTTGGTCA  
 CAACTGTAACATTCTTATTGACCAATTCATGAATCAAAAAAGCAGTTGTTGTTCCCAGCA  
 TCCGATAAAGATGACATCTTTTTTCCTTTAATGAGAGAGGCTGCTTTCTGAGCCAGCAATT  
 TCTTTTCTTGAAGGTTTTTGACAGATTTTTCTTG

## ORF Predictions:

ORF #	Start	End	Direction	Length
-----	-----	-----	-----	-----
6	505	1170	R	222 aa

[SEQ ID NO: ] 3864482-6 ORF translation from 505-1170,  
 direction R  
 VAEDTRINVKIXADQETEINGTGPTVEPVKLEELKAILSSLTAEDTVVFAGSSAKNLGNV  
 IYKDLISLTRQTGAQVVCD FEGQTLIDSLDYQPLLVKPNNHELGAIFGVKLESLDEIEKY  
 ARELLAKGAQNVIISMAGDGALLVTSEGAYFAKPIKGTVKNSVGAGDSMVAGFTGEFVKS  
 KDAVEAFKWGVACGTATTFSDDLATAEFIKETYGKVEVEKR\*

## Blastp and/or MPSearch Result:

## Description:

1-PHOSPHOFRUCTOKINASE (EC 2.7.1.56) (FRUCTOSE 1-PHOSPHATE  
 KINASE). - RHODOBACTE R CAPSULATUS (RHODOPSEUDOMONAS  
 CAPSULATA).

Assembly ID: 3864496

Assembly Length: 1975bp

[SEQ ID NO: ] 3864496 Strep Assembly -- Assembly  
 id#3864496  
 TCAAAGAGTAACAAAGGCACCAAATTCTCGATAGGAACGATTTAGCACGGTAAACTTCAT  
 CCACTTGGGTTACGGAACCAACCAGCAATAATTTCTTTGGGCACGGGTTAATAGCATT  
 TTGGTCAACTAGGAGTAGATAGAACACATTTCTNTTCTTCGTCTATATCAATCTTAACACC  
 TGTTTCAGCGATAATCTTGTCGATGGTTTCTCCACCCTTACCGATGACAATCTTAATCTT  
 GTCCACATCAATCTTGATCGTATCAATTTTCGGAGCAGTTGGAGCCAATTCTGGACGAAC

TTCTGGAATGGTTGCTTCAATGACATCAAGGATTTCAAAACGCGCTTTCTTGGCTTGAGC  
AAGAGCCTCCGTCAAGATTTCTGCAGTAATCCCTTGAATCTTGATATCCATTTGAAGGGC  
TGTAATCCCATCACGAGTACCTGCAACCTTGAAGTCCATATCTCCAAAGTGATCTTCCAA  
ACCTTGGATATCTGTCAATACTGTGTAGTTATTTCCATCTGAGATAAGTCCCATAGCAAT  
ACCAGCTACTGGCGCCTTGATTGGCACACCACCAGCCATAAGGGCAAGAGTTCCCGCACA  
GATAGAAGCTTGAGATGAAGAACCGTTTGATTCCAAAACCTTCTGCTACTAGACGGATAGC  
GTATGGGAATTCTTCCAAGCTTGGCAAGACTTGAGCAAGAGCACGCTCACCAAGGGCACC  
GTGACCGATTTTACGACGACCTGGCGCACCGTAACGACCTGTTTCCCCTACAGAATATTG  
AGGGAAGTTATAGTGGTGCATAAAGCGTTTCTTGTACTCTGGATCCAAACCATCAATGAT  
TTGAGTTTCTCCCATCGGAGCCAAGGTCAAGACTGAAAGAGCTTGAGTTTGGCCACGAGT  
AAAGAGACCTGAACCATGTACACGAGGAAGGAAGTCAACAACCGCATCCAAAGGACGGAT  
TTCATCGACCTTACGACCATCAGGACGCACCTTGTCTTCTGTAATTAAACGTCGCACTTC  
TGCGTGTTCATTTGTTCCAAGATTTTCAGCCACATCACGCATAATACGGTCAAATTCTTC  
GTGGTCCGCATATTTTCTTCGTAAACGGCAGTCACTTGGTCTTTCACTGCTTGAGTTGC  
AGCTTCACGGGCCAATTTCTCTTATACTTGAAGTGCCTTTTGGAGGTCAGTGTGTAGGC  
TGCAATGATTTTCAGCTTGCAATTCAGCATCCACGTGAAGCAATTCCACTTCTGCTTTTTTC  
TTTACCGACAGCAGCAACGATTTCTTCTTGGAAGGCAATCAATTCTTTGACAGCTTCGTG  
CCCTTTAAGAAGCGCTTCCAACATGATTTCTTCTGACAATTCTTTGGCACCAGACTCTAC  
CATGTTGATAGCGTGCTTGGTTCCAGCTACTGTCAATTCAAGAAGAGATTGCTCTGCTTG  
TTCTTGACTTGGGTTGATGATGATTTGGCCATCTACATATCCCACTTGTAACCCAGCAAT  
TGGTCCGTCAAATGGAATATCTGAAATAGACAGTGCCAAAGATGAACCAAACATAGCAGC  
CATTGGTGCAGATGCATTTTCATCATAAGAAAGCACTGTATTGATGACTTGGACTTCATT  
ACGGAAACCTTCCGCAAACATAGGACGAATCGGACGGTCAATCAAACGCGCTGTCAAGGT  
CGCATCTGTTGAAGGACGTCCTTCACGTTTCATAAAGCCACCAGGAACTTCCCAGCCGC  
ATACATTTTTTCTTCGTAGTTGACTTGGAGTGGGAAGAAATCCCCAGTTGCCATTTTCTT  
AGACATAACGGCAGCAGTCAAGACAGTTGACTCACCGTAACGTACGACAACAGATCCATT  
TGCTTGCTTAGCAACCTGACCAGTCTCTACAATTCGATCACGACCCGCAAAAGTCGTTTG  
AAACACTTGTTTTTGCCATTTTAATCCCCCTTTGGATTGATGAAATTATACGCCTTG

## ORF Predictions:

ORF #	Start	End	Direction	Length
6	1	1128	R	376 aa

[SEQ ID NO: ] 3864496-6 ORF translation from 1-1128,  
direction R

VKDQVTAVYEEKYADHEEFDRIMRDVAEILEQMEHAEVRLITEDKVRPDGRKVVDEIRPL  
DAVVDLFLPRVHGSGLFTRGQTQALSVLTLAPMGETQIIDGLDPEYKKRFMHYNFQYSV  
GETGRYGAPGRREIGHGALGERALAQVLPSEEFPPYAIRLVAEVLESNGSSSQASICAGT  
LALMAGGVPIKAPVAGIAMGLISDGNNYTVLTDIQGLEDFGDMDFKVAGTRDGITALQM



DIKIQGITAEILTEALAQAKKARFEILDVIEATIPEVRPELAPTAPKIDTIKIDVDKIKI  
VIGKGGETIDKIIAETGVKIDIDEEENVFYLLLVQDQAINPCPKLLLLVWFREP KWMKFT  
VLNRSYREFGAFVTL\*

Blastp and/or MPSearch Result:

Description:

polynucleotide phosphorylase (pnp) homolog - Haemophilus  
influenzae (strain Rd KW20)

Assembly ID: 3864514

Assembly Length: 1678bp

[SEQ ID NO: ] 3864514 Strep Assembly -- Assembly  
id#3864514

CTCATGTTTGATTTTTTAAACCAAGAAAACTGCTAATAGTAAGTAAGGATAAAAAAGAAA  
TAGTATGCTATATAAGAGAAAAAAATCCTATAAAGAACTAGCATTGTTTGCAATACTT  
ATACCATAAAATTCTCTTAAAAATCAACCTCCTTTATCTCCAAAGAGAAGCTAAACCA  
TTACTAAATGCAATCAGAAAAATCAATAAAAAATAAAGTCGCCGTCCAAATCCCCGTACTA  
AGAGCTGCTAATTTGAAACTAAACTGGTAAAGTGCTTAATTGATTTTCAGACGAATACGA  
CACTCCAACCTATTAAAATAGTTATTCATCAAATAAAAAAGAATAATATATATGTGAAC  
GGAAAGCAATATACTCCAGTCGTCATATCTTGAAGTAAACTAAGATCCATTCTAATACA  
TTTGATGATGGAATATTTGGCGACAGCGCAATAAATATACTGTACTAGATAAAACACAG  
GATAGCAGTAATATAAAATAAACCAATACTGATAAAAAATCTTTTTTGTAATTTGAACA  
AATTGTTTTCATTATACATAGTCCTCTGAATGTAGAAAAATGTACCATAAAACAACCAAC  
AACTAACAAATAAAATAAAAGCAAGATGCCCACCTAACTAAGGAAAGACTGATATCTTTCT  
GATATCCCAAAGCTAATGTTGTCACAGGTTCTAAGTAAGATAGCCCTAAAAATAGCCCCAA  
AAATACCACCAACCATCATATAGGCAACTGGGATGAAAATAGCTCCTATTTTTTTCTTCA  
CTAGCAAAGCACTAGCTAGTCCAAAAATAGAGAACACAGCGCCCCAACTCCATACCAGA  
GAGTCGTCACAAGACTATAGAGCAACTGATTAGAATCAAATAATTCTTTTAAGGCACCAC  
TATAATCTCCAATATAAAATTTCTGATAAGGAGTCACTAAAAGATTAATTCCTAATAATA  
ATAAATAGGGGAGAAAAAGACTAGAAAAGAAGAAATAATTGCAGTACTACCTACAATAG  
CCAGATACTTCTTTTTAGAAATTCGGCACAAATTGTGCTGTTAGAAAATGACTCTCAGCAT  
CCTCTATTATCTGACTAGAATAGGGCAGTGCTACAGATAAGTGCAGCTACTAGGCTAATCG  
GTGAAAATCCTCGAATAGAAGAAGCGGCAAAAAAATCGATAAACCTTCAATTTTATAAA  
TACCATTGAAAGCAAGGAAATTTCTTAACTCATGCAAAGAAGGGTCAAAAAATAAGACA  
TATAAAATCGAGGTGATTGAACGACTCCGTACAAGATTACAAATGAAAAATCCATCCTT  
ACTCCTCCTTATAATAAAAAATAGGGTGTAGCATTTCTTTTTTCATGCTACACCCACAATCA

ACCATCTTTAAGGCTTACTCTGACAAGTAAGTTAATAAGAATCTGGACTCCAAGAACCTG  
 AAGTATGAATTCTTACATGATTTCCAAATTGTGGCGCCATAGCTAATCTAGTACCAGAAC  
 CAATATAATTGTCACCACCTCCATTATAGTACATGACAATCCTAGAGCCAGACCCCAATG  
 AATATACCGGGGTAATATCTGACCCACTATAGGCGCTACGAATAGAGGTACTTAACCTTT  
 TACCGCCACCAGTGCTGTCACTGTTATTAATTCCAGCAGAGGCGTTTTCTTTCTCAAG

## ORF Predictions:

ORF #	Start	End	Direction	Length
6	551	937	R	129 aa

[SEQ ID NO: ] 3864514-6 ORF translation from 551-937,  
 direction R  
 VTPYQEIIYIGDYSGALKELFDSNQLLYSLVTTLWYGVWGAVFSIFGLASALLVKKKIGAI  
 FIPVAYMMVGGIFWAILGLSYLEPVTTLALGYQKDISLSLVSGHLAFILFVSVCLVVGTF  
 FLHSEDYV\*

## Blastp and/or MPSearch Result:

Description:  
 unknown

Assembly ID: 3864518  
 Assembly Length: 2908bp

[SEQ ID NO: ] 3864518 Strep Assembly -- Assembly  
 id#3864518  
 CTGGTGAAGTTGACTGAGACCGAAGCGATAGGCATCCATGATAATCAAGACAGTCGCACT  
 GGGAACGTTGACCCCAACCTCAATAACCGTCGTCGAAACCAGAATATCCGTCTTTCTCTC  
 CTTGAAATCCTGCATGATCTGGTCTTTTCGTCACCTTTCATCCTACCATGTAAAAGAGC  
 CACCTCTGTCTCGCCTGCAAAATGAGTCGTCAACTCCTCTGATAAGGCAATGGCATTTTT  
 CAAATCTAGAGCTTCTGATTCTTCAATCAAAGGAGAGATGACATAGACTTGGAACCTTT  
 TTGAATTTCCCCCTCTAACCAAGTCAAGACCTGAGGTAGTTGCTCATGTTTGATCCAGCG  
 CGTCACAATAGGCTTCCGACCTGCTGGCATCTGGTCGATAATGGAAACATCCATATCTCC  
 AAAGGCTGTGATGGCAAGCGTCCGTGGAATGGGAGTCGCCGTCATCATGAGGACATCTGG

ATTGTCGCCTTTTTCCCGTAAAATACGCCTTTGCCCTACACCAAAACGGTGCTGCTCATC  
GATAATAATCAAACCAAGACGAGCATACTCCACCCCATCTTGATCAGAGCGTGAGTTCC  
TATAATCAAATCAGCCTCACCTTGGCAATGGTCTCCAAGACTTCTCTCTTTTCTGCAGC  
TTTCAAGGAACCTGTCAAGAGAGCCAGTTTCAAATTGGGAAAAAGGTTCTGTAAACTCTC  
AAAGTGTTGCTCTGCGAGGATTTCTGTTGGTACCATTAGGGCAGCCTGATAACCTGCTGT  
CACTGCCGCAAACATGGCCAAGCCAGCGACTACCGTTTTTCCGCTCCCCACATCTCCTTG  
TAGGAGACGATTTCATGTGGTGGTCCGACTTCATATCAGTTAAAAATTTCTTGCAAACCTTT  
TTCTTGAGCTTGGGTCAGGGCAAAGGAAGACTTGCTTTAACTGCTGTCACTTTTTCTTG  
AGACCAATCCAGAACCAGACCACTTCCCTGAACTCTATTTTCAGACTTGAGCGTCTGCAG  
CTGCATTTTGAAATAAAAGAGTTCTCTCAAACCTTGATACGGCGAAGAGCCTGCTTGTATTC  
TGCCAAATCCTTTGGAAAATGCATAGCTCGGACTGCCTGACAACGGGACATGAGTTTGTA  
TTTGTCTAGTAAAGACTGGGGCAGATTTTCTTCTATCAAGAGGTCCAGTCCCTGATCAAA  
AGCCGTCTTGATGACCTTGACCAGACTGGCCTGACTGATTCCCTGAGCCAGACGATAGAC  
AGGCTGGAGGTCATCTTCTACCTGAGCCAGAACCTTCATCCCAGTCAGACTAGCCTTAGC  
GCGGTCCCATTTTTCCAAAGACAGCAAGGGTTGCTCCCAACTCTATTTTATCAGCCAGATA  
GGGCTGGTTAAAGAAATTCACCGCAAAAACGACCTCTCCCTGCTTGAGACTAAAACGCAG  
GCGATTGCGCTTGAAACCATAATACTGGACACTAGCAGGAGTCACTACCTGACCAGAAAG  
AACTGCCTTCTCACCGTCTTCTAGTTCCAGCACCTGCTTGGTTTTGAAGTCTTCATAACG  
GAAAGGAAAGTAGAGCAAGAGATCTTGCAAGTTTTTCAATTCCTAGTTTGGCGTATTTTTTC  
TGCTGACTTTGGTCCCACACCAGGCAAGACATGCAAGGGTTGATGTAGATTCATGCTCCA  
CTCCTTTCTTTTCTAATAATATTCTCTCGGAATACGGTCGCTGAGGAGGCAAACCACCTC  
ATAGTTAATGGTTACGCGGTAGGTGCTACCTGAGTTGCAGTGATTTCTTTATCCCCATT  
GGAGCCAATCAAGGTTACCTTGGTTCCTAGCGGATAAAGCTTAGGCAATCGAATAGTGAT  
TTGGTCCATCGAAACCCTGCCGACAATTGGGCAAGCTTGGCCATCTACCAAGACAGAGAA  
ATTTTGCATGTCTCTTGTTCCATCCATCTGCATACCCGATTGGCACGGTCGCGATGACTTG  
CTCGCTATCCGCTTGATAAGTTGCTCCATAGCCCATGCAAGCTCCAGCTGGAACGTGCTT  
GACATGAAACCAGAGCAGACTCCAAGGTCAAGGCCGGTATCAAATCATAAGGCAAATTCA  
AGACCGCTCCACTTGGATTGAGGCCATACATGGCATCTCCCATACGAACCGCATTGAAAA  
TAGTCTCTACATGCCAAAAAGTCGTTGCAGAATTGCTAGCATGAACCAGCTCTGGAACCT  
CCTTCATACTAGCTAAAATAGTATTAAACCGTTCTAACTGGGCATTAAAATAGTCATCTG  
ATTCTCATCAGCAGTAGCAAAGTGGGTAAAGATTCTTCAACACGAACACCGTGTTGTT  
GGGAGCAAATCTTGAGCCTGCTCAACCTCACTGGCCTCTCTAAAACCAATCCGTCCCATC  
CCTGAATCAATCTTGAGGTGGACTGTCAATCCAGTTAGGTCCACTTCCTTATCTAAGAGT  
GCTTGGAATCCACTCCAGTCCAGCCACTGTCAAGGTGAAGTCATATTCTTTAGCTAGAAG  
CAACAGCTTGTCTGAGTTCAATGGCTTCATCAAACCTCCTAAAATGAGGATTGGCTTGCTG  
AGTCCAGCTTGTCTGAGTTCAATGGCTTCATCGATATTGGAAACGCAAAAGCCATCAACA  
TCATCTTGAATTGCCTTGGCAACGGCAACAGCTCCATGGCCATAAGCATTGGCCTTGACC  
ACAGCCCACTTGAGCGTTCCTTGAGGGATATGAGCCCCCATTTGCTGAATATTTTGTGCA  
ATAGCTCCCAGATGAATCAGAACCTTGGTTGGTCTATGTTGGACTAACTTTTCATGATTTT  
CCCTCCAAAATGACACTGGCTGTCAAACTGATCGGTGTTGGCTGAATAAACAGCCAAA  
TCTTTTCCTGAAAAATGGTGGCCTGACT

## ORF Predictions:

ORF #	Start	End	Direction	Length
8	1985	2371	R	129 aa

[SEQ ID NO: ] 3864518-8 ORF translation from 1985-2371,  
direction R

VRLSRLKICSQQHGVRVEGIFTHFATADEESDDYFNAQLERFNTILASMKEVPELVHASN  
SATTFWHVETIFNAVRMGDAMYGLNPSGAVLNLPYDLIPALTLESALVSCQDSSSWSLHG  
LWSNLSSG\*

## Blastp and/or MPSearch Result:

## Description:

ALANINE RACEMASE (EC 5.1.1.1). - BACILLUS  
STEAROTHERMOPHILUS.

Assembly ID: 3864522

Assembly Length: 1549bp

[SEQ ID NO: ] 3864522 Strep Assembly -- Assembly  
id#3864522

CCAGTTAAGGCTGGTTGTCGTTTCCTTCTGGTAAAGAGAACTTCCTTTGTAGAGCCTGCAT  
TAATAAACTTACGAATGGTTTCACGAGCAGCTTCATAAGGAAGCTGTCGCTCGTTCCGCT  
AAGGTATGGACACCACGGTGAACATTGGCATTGTCTGCTCATAGTAACTGTTAATAGCT  
TTCAGAACTACTAGTGGTTTTTGTGTGTCGTCGAGCATTGTCCAGATAGACCAGAGGTTCA  
TCATTGACAATCTGATCTAAAATTGGAAAATCCTTGCGAATCGCTTCTACATCTAACATA  
GGCTTCCCCTTAGCGTTTTGACAATTTCTCTTCGATAGTTGCAATCATTTTCATCACGAAC  
TTCCTTGACTGGAATCTCCACGATAACAGATCCAAGGAAACCACGAACAACCAAACGCTC  
TGCAGTTGCCTTATCCAATCCACGACTCATGAGGTAATACATGTCTTCTGGATCAACTTG  
TCCGATAGACGCTGCGTGTCTGTCAGTGACATCATTTTCATCAATCAAAAGAATTGGGTT  
AGCATCTGAACGCGCTTGGTCTGAAAGCATGAGAACACGGCTCTCTTGTGTGCGCATCTGC  
TCCCTTAGCACCTTGATGATGTGGCCGATACCATTGAAAGTCAAAGTTGCTTTTTCAAG  
GATAACCCATGTTGTAGGATATTTCCGATAGAGTTGCAGCCATAGTTAGTTACACGAGT  
ATCAATCCCTTGTACCTGACGACCACTTGAAAGAGCTACAACCTTGAGGTCAGCATGGCT  
ACCATTACCAATCAAGTCACTATCAAAATCAGCAACGACATTCCTTCGTTTCATGACACC

GATAGCCCAGTCAATACTTGCATCGTTGCCTAATTCCATACCACGACGGCTAATGTAGGC  
 AGTGACGTTTTTCACCTAGACGGTCGATAGCAGCAAACCTTGACTTGCGCACCAGAACGTGC  
 AATCACTTCCACTGTGATATTGGCAGTTACTTTGTCACTTCCTTCACCGCGTGACTCTAA  
 ACGCTCCAGATAACTAATCTTAGAATTTTTTACCAGCGATAATCATAATATGCTTGTTAAA  
 CGGCACATTGCTATCGCTATCTTGGTAGAAAATTCCTTCAATTGGCTCTGTGATTTCTAC  
 GTTATCTGGAATATAGAGTACAGCACCACTGTAAAGTAAGCTGTGTGGTAAGCCGCCAA  
 CTTGTCATCATCATACTTAACAGATGACATGAAGAATTCTTCGATCAGCTCTGGAATTTC  
 TTCTAAAGCTGAGTGAAAGTCTGTGAAGACAACACCCTGTTTCAGCTAACTCAACTGGAGT  
 TTGTTGCGAAAACAGTTTGAGTTCCTACTTGCACCAACTTCAAGTGATGATCTAAAGCTGT  
 GAAATCTGGAACATTTGCTGATGGCTCATTTCTGTAAATCGTTCCATCACCCAAATTCCA  
 ACGGGTGGAATTTGACACGCTCAATAACTGGTAATTCCAAAGTCTCAATCTTGGTCAAAA  
 AGCTTTTTGACGGAAATCAGCCAACCAAGCTTGGTTCCAGCGGTGCATT

## ORF Predictions:

ORF #	Start	End	Direction	Length
7	310	1458	R	383 aa

[SEQ ID NO: ] 3864522-7 ORF translation from 310-1458,  
 direction R

VSNSTRWNLGDGTITGNEPSANVPDFTALDHHLKLVQVGTQTVFEQTPVELAEQGVVFTD  
 FHSAL EEIPELIEEFFMSSVKYDDDKLAAYHTAYFNSGAVLYIPDNVEITEPIEGIFYQD  
 SDSNVFPNKHIMI IAGKNSKISYLERLESRGE GSDKVTANITVEVIARSGAQVKFAAIDR  
 LGENV TAYISRRGMELGNDASIDWAIGVMNEGNV VADFSDSLIGNGSHADLKVVALSSGR  
 QVQGIDTRVTNYGCNSIGNILQHGVILEKATLTFNGIGHI IKGAKGADAQQESRVLMLSD  
 QARSDANPILLIDENDVTAGHAASIGQVDPEDMYLMSRGLDKATAERLVVRGFLGSVIV  
 EIPVKEVRDEMIATIEEKL SKR\*

## Blastp and/or MPSearch Result:

Description:  
 unknown

Assembly ID: 3864568  
 Assembly Length: 1548bp

[SEQ ID NO: ] 3864568 Strep Assembly -- Assembly  
id#3864568

CTTGGTAGAACTTGCTAATCAAGCTGGCAAGCCTGTAGTCTTGGACTGCTCAGGTGCAGC  
ACTTTCAGGCTGTTCTTGAATCACCCCATAAACCAACAGTCATCAAACCAAATAATGAAG  
AATTGTCTCAGCCTTCTTGGAAGAGAAGTTTCTGAGGATTTGGATGAATTAAGAAGTA  
CTTCAAGAAACCTTTGTTTGCAGGGATTGAATGGATTATCGTTTCACTTGGTGCCAACGG  
TACTTTTGCCAAACATGGTGACACTTTCTACAAGGTAGATATTCCTAGAATTCAGGTGGT  
AAATCCTGTTGATCTGGAGACTCTACTGTGGCAGGAATTTCTTCAGGACTTCTTCACAA  
AGAAATCGGATGCAGAATTACTCATCAAGGCAAATGTCCTTGGTATGCTCAATGCTCAAGA  
AAAAATGACTGGTCATGTCAACATGGCCAACTATCAAGTTCTATATGATCAATTAATAGT  
AAAAGAGGTATAAAATGGCTTTAACAGAACAAAAACGTGCACGCTTAGAAAAACTTTCTG  
ATGAAAATGGTATCATCTCAGCTCTTGCAATTTGACCAACGTGGTGCTTTGAAACGCCTCA  
TGGCTCAACACCAACAGAAGAACCAACTGTGGCTCAAAATGGAAGAACTGAAAGTCTTGG  
TAGCAGATGAATTGACTAAATACGCTTCATCAATGCTTCTTGACCCTGAGTATGGACTTC  
CAGCAACTAAAGCTCTTGATGAAAAAGCTGGTCTTCTCCTTGCTTATGAAAAACAGGTT  
ATGACACAACAAGTACAAAACGCTTGCCAGACTGCTTGGATGTTTGGTCTGCAAAACGTA  
TTAAAGAAGAGGGTGCAGATGCAGTTAAATTCTTGCTTTACTATGATGTAGATAGTTCAG  
ACGAATCAACCAAGAAAAACAAGCTTATATCGAGCGTATCGGTTCTGAGTGTGTGGCTG  
AAGATATCCCATTTCTTCTTGAAATCCTTGCTTACGATGAAAATCGAATTGCAGACGCAG  
GTTCTGTAGAATATGCGAAAGTAAAACCAACACAAAGTTATCGGTGCTATGAAAGTCTTTT  
CAGACCCACGCTTTAACATTGATGTCTTGAAAGTTGAAGTTCCTGTTAACATTAAATATG  
TTGAAGGCTTCGCTGAAGGTGAAGTGGTTTACACACGTGAAGAAGCAGCAGCCTTCTTCA  
AAGCGCAAGATGAAGCAACGAACCTTGCCATACATTTACTTGAGTGCTGGTGTATCAGCTA  
AACTCTTCCAAGATACTCTTGTATTGCTCATGAATCAGGTGCAAACTTTAACGGAGTTC  
TTTGTGGCCGTGCTACATGGGCAGGATCAGTTGAAGCTTACATCAAAGATGGTGAAGCAG  
CAGCTCGCGAATGGCTTCGCACAACTGGATTGAAAACATTGATGAGCTCAATAAAGTTC  
TTCAAACAACAGCGACTTCATGGAAAGAACGTGTGTAAGAAAGTCCTCCTAGTTTtaggaa  
CATGAATCTAAAAAAATTCAAAAAAAGTTGTATGTAAAGGTTTACAAA

#### ORF Predictions:

ORF #	Start	End	Direction	Length
6	296	493	F	66 aa

[SEQ ID NO: ] 3864568-6 ORF translation from 296-493,  
direction F  
VVNPVSGDSTVAGISSGLLHKESDAELLIKANVLGMLNAQEKMTGHVNMANYQVLYDQL  
IVKEV\*

Blastp and/or MPSearch Result:

Description:

TAGATOSE-6-PHOSPHATE KINASE (EC 2.7.1.-)  
(PHOSPHOTAGATOKINASE). - LACTOCOCCUS L ACTIS (SUBSP.  
LACTIS) (STREPTOCOCCUS LACTIS).

Assembly ID: 3864590

Assembly Length: 1360bp

[SEQ ID NO: ] 3864590 Strep Assembly -- Assembly  
id#3864590

CTTCCTCCAGCAAAATCCACTGCTGAGAAGCTAAAGGGAGCGTGAGATAGCCCTCTTTCT  
CTACTGGTTGGTCTGAAATCCGAGCCTCAGGAAACCAGTCTTGTAGTTCTTTTTCCCTCA  
TGTTCTAGCCCTCCACTTTTTGGATGCACCATGAAACCAAACCTCTCAAGACGTTCCAGAT  
TCTCAGTCATATGGAGATAGCCATAACCGCTTCAAATCCCGTGACATACGATAAGTCA  
CGACATCTGCATTTTTAGCCTTTGTGTGGCTATTGGTATTGCGGCCACGTTTGTAGATTT  
CTTCTTCTTTTTCCGTTAGGACCTGCTCCTCCAACATGAGAGCAATCAGGCGAGCCTGAG  
CCTTGGCTGACACATACTTGGTTGCTTCTTGATGGAGTTTATTGGGTTTGGTCATACCTT  
TGAGGATGAGGTGACGGCGAATATACATAGAATACACCGCATCCCCCTCAAAGGCTAGCG  
CAATCCCGTTAATGAGATTGACATCAATCACGTGTCCACCTCACTCCATCCTTGGTATCA  
AGGAGCTTAATTCCTTGAGTAACCAATTGGTACGGATTTGGTCTGCTGTCTCAAAGTCT  
CGATTGGCAGCGCCTCTTGGCGTTTTTGAATCAAGTCTTCAATCTCTGCATCCAAAAC  
TCCTCAACAAAGACAATTCCAAAAATTTCTAACATATCTGCAAGAGCTTGCTTGACACTT  
GCATCATAGTTCCCTGAGTTGATCCATTTGGCCATTTCAAAGACAACCTGTGATAACCGTTG  
GCAGCATTAATAATCTTCATCCATAGCTGCTACAACTTATCTTTAAAGTTTGTAACTCT  
TGGGCATCCACGTTTCTGTAAATGGTTGTTTCGTAAGTATTCTTCAGATACTTGAGATTG  
GTCTCGGCATCGCGAACTGCCTTTTCCGTGAAGTTGATAGGCTTACGGTAGTGCTGGGTC  
GCAAAGAAGAAACGAAGTACTTGCCCATCAAGAGTTTTAAGGGCATCGTGTACCGTAATG  
AAGTTACCCAAGGACTTAGACATTTTGACATTGTGATATTGACAAAGCCATTGTGCATC  
CCAGTTAGTTAGCAAAAGCCTTGCCGTGTTTGTAGCTTCAGATTGGGCAATTCATTGGTGT  
GGTGTGGAACTCTAGGTCAGCTCCACCACCGTGGATATCAATGGTATCACCTAAAATCT  
CTGTGACATGACTGAACACTCAATATGCCAACCCGGACGTCCAGGTCCCCAAGGACTAT  
CCCAAGAAATCTCACCTGGTTTGGGAAGATTTCCATAAAGCAAAGTCTACAGGATTTTCCT  
TACGAGCCGTTTCTTCATCGGTACGACCTGAAGCACCTAG

ORF Predictions:

ORF #	Start	End	Direction	Length
-----	-----	-----	-----	-----
6	125	511	R	129 aa

[SEQ ID NO: ] 3864590-6 ORF translation from 125-511,  
direction R  
VIDVNLINGIALAFEGDAVYSMYIRRHLLKGMTKPNKLHQEATKYVSAKAQARLIALML  
EEQVLTEKEEEIYKGRNTNSHTKAKNADVVTYRMSTGFEAVMGYLHMTENLERLESLSV  
WCIQKVEG\*

Blastp and/or MPSearch Result:

Description:  
unknown

Assembly ID: 3864596  
Assembly Length: 2130bp

[SEQ ID NO: ] 3864596 Strep Assembly -- Assembly  
id#3864596  
TTGACAAACGGTACTTATGTTAGTGGACAGCACTATCGGAGCAGGAGCGGTCATTACCAAT  
TCTATGATTGAGGAAAGTAGTGTGTCAGACGGTGTGACAGTCGGTCCTTATGCTCAACAT  
TCGTCCAAATTCAGTCTGGGTGCCCAAGTTCATATTGGTAACTTTGTTGAGGTGAAAGG  
ATCTTCAATCGGTGAGAATACCAAGGCTGGTCATTTGACTTATATCGGAAGCTGTGAAGT  
GGGAAGCAACGTTAATTTTCGGTGCTGGAAGTATTACAGTCAACTATGACGGCAAAAACAA  
ATACAAGACAGTCATTGGAGACAATGTCTTTGTTGGTTCAAATTCAACCATTTATGCACC  
AGTAGAACTTGGTGACAATTCCTTCGTTGGTGCTGGTTCAACTATTACTAAAGACGTGCC  
AGCAGATGCTATTGCTATTGGTCGCGGTTCGTCAGATCAATAAAGACGAATATGCAACACG  
TCTTCCTCATCATCCTAAGAACCAGTAGGAGCCTATCATGGAGTTTGAAGAAAAACGCT  
TAGCCGAAAAGAAATCTATCAAGGACCAATATTTAAACTGGTCCAAGATCAGGTTGAATT  
ACCAGAAGGCAAGGGAAGTGGCCCAACGGGATTTGATTTTCCACAATGGGGCTGTCTGTGT  
TTTAGCAGTAACGGATGAACAAAACTTATCTTGGTCAAGCAGTACCGCAAAGCTATCGA  
GGCTGTCTCTTACGAAATTCAGCCGGAATTTGGAAGTAGGAGAAAACACAGCCCCTGT  
GGCAGCTGCCCTTCGTGAATTAGAGGAAGAAACAGCCTATACAGGGAAATTAGAAGTCTT  
GTACGATTTTTATTAGCTATTGGCTTTTGTAAATGAGAAGTTAAAAGTATATTTAGCAAG  
CGATTTGACAAAAGTGGAAAATCCGCGTCCGCAGGATGAGGATGAAACCTTGGAAGTCCT



TGAAGTGAGCTTAGAAGAAGCGAAAGAATTAATCCAATCAGGTCATATTTGTGATGCCAA  
 GACAATTATGGCTGTTTCAGTATTGGGAGTTGCAGAAAAAATAGAGGAGGTCAGTATGGGT  
 AAATCTTTATTAACGGATGAAATGATTGAAAGAGCTAATAGAGGCGAAAAAATTTTCAGGT  
 CCTCCTTTGCTAGATGATAATGAGGAACTAAGATTTTACCAACCTCTTCTTCCCGTTTT  
 GGTATGCCAATCCTAAGGATCATGGTTTTAGCCAGGAAACCTTGAAGATTCAGGTCGAA  
 CCATCTATTTCATAAAAGCCGTCGTATTGAAAATACCAAGAGAAATGTCTTCAATTCTAAG  
 TTGAATAAAATCTTATTTGCGGTCATCTTCTCTTGATTTTGTCTGTTTTAGCAATGAAA  
 CTTTTGTAATAGAAAAGGAATTGAAATGAAAATAGGAATTATTGCTGCTATGCCAGAAGA  
 ACTGGCTTATCTGGTCCAGCATTTAGATAATGCCCAGGAGCAAGTTGTTTTGGGGAATAC  
 CTATCATACAGGAACCATTGCTTCTCATGAAGTCGTTCTTGTAGAAAGTGGAATTGGTAA  
 GGTATGTCTGCTATGAGTGTGGCGATTTTGGCTGATCATTTCCAGGTGGATGCCCTTAT  
 TAATACGGGTTTCAGCTGGGGCAGTAGCAGAAGGTATCGCTGTTGGGGATGTCGTGATTGC  
 TGACAAATTAGCCTATCATGACGTGGATGTCACAGCTTTTGGCTATGCTTATGGACAAAT  
 GCGCAACAACCGCTTTATTTTCGAATCAGACAAACCTTTGTTGCTCAAATCCAAGAGAGT  
 TTATCTCAATTGGACCAAACTGGCATCTTGGTTTGATTGCTACAGGAGATAGTTTTGTT  
 GCAGGAAATGACAAGATAGAAGCGATTAAAGTCCCATTTCAGAGAGTTTTCAGCGTGGAG  
 ATGGAGGGGGCAGCTATTGCTCAAGCAGCGCATGCCCTCAATCTCCAGTCTTAGTCATC  
 CGAGCTATGAGTGACAATGCCAACCATGAAGCAAACATCTTTTTTGATGAGTTTATTATC  
 GAAGCTGGACGTCGCTCTGCCCAAGTCTTGTGGCCTTTTTGAAGGCTTTAGATTAAGCG  
 GAAATTTGACAGTTTTTCTAGATCAAGCTT

## ORF Predictions:

ORF #	Start	End	Direction	Length
11	1915	2097	F	61 aa

[SEQ ID NO: ] 3864596-11 ORF translation from 1915-  
 2097, direction F

VMEGAAlAQAAHALNLPVLVIRAMSDNANHEANIFFDEFIIEAGR RSAQVLLAFLKALD  
 \*

## Blastp and/or MPSearch Result:

## Description:

PFS PROTEIN (P46). - ESCHERICHIA COLI.

Assembly ID: 3864624

Assembly Length: 2128bp

[SEQ ID NO: ] 3864624 Strep Assembly -- Assembly  
id#3864624

ATCGAATTTGAGTTTGTAGGCTTGGATAACTATATCCGTATGTTTAAAGATCCTGTCTTT  
ACAAAATCTCTGATTAACACAGTTATTTTGGTTATTGGATCTGTACCAGTTGTTGTTCTA  
TTCTCACTCTTTGTAGCATCTCAGACCTATCATCAAAATGTCATTGCCAGATCCTTCTAC  
CGTTTCGTCTTCTTCCTTCCTGTTGTAACGGGTTAGTGTTGCCGTGACAGTTGTTTGGAAA  
TGGATTTATGACCCACTATCAGGGATTCTAAACTTTGTCCTTAAGTCAAGCCACATCATC  
AGCCAAAACATTTCTTGGTTGGGAGATAAAAACTGGGCATTGATGGCGATTATGATTATT  
CTCTTGACCACTTCAGTTGGTCAGCCCATCATCCTTTATATCGCTGCCATGGGGAATATT  
GACAATTCAGTGGTTGAAGCGGCGCGTGTGATGGTGCAACTGAGTTTCAAGTTTTTTGG  
GAAGATTAAATGGCCAAGCCTTCTTCCAACAACCTCTTTATATTGCAATCATCACAACAAT  
TAACTCATTCCAGTGTTTCGCCTTGATTTCAGCTTTTGACATCTGGTGGTCCAACTACTC  
AACAAGTACCTTGATGTACTACCTTTACGAAAAAGCCTTCCAATTGACAGAATACGGCTA  
TGCCAACACAATTGGTGTCTTCTTGGCAGTCATGATTGCTATCGTAAGCTTTGTTCAATT  
TAAAGTACTTGGAACGACGTAGAATACTAAAGAAAGGAGACAGCTATGCAATCTACAGA  
AAAAAAACCATTAACAGCCTTTACTGTTATTTCAACAATCATTTTGCTCTTGTTGACTGT  
GCTGTTTCATCTTTCCATTCTACTGGATTTTGACAGGGGCATTCAAATCACAACCTGATAC  
AATTGTTATTTCCTCCTCAGTGGTTCCCTAAAAATGCCAACCATGGAAAACCTCCAACAAC  
CATGGTGCAGAACCTGCCTTGCAATGGATGTGGAACCTCAGTATTTATCTCATTTGGTAAC  
CATGTTCTTAGTTTGTGCAACCTCATCTCTAGCAGGTTATGTATTGGCTAAAAACGTTT  
CTATGGTCAACGCATTCTATTTGCTATCTTTATCGCTGCTATGGCGCTTCCAAAACAAGT  
TGTCCTTGTACCATTGGTACGTATCGTCAACTTCATGGGAATCCACGATACTCTCTGGGC  
AGTTATCTTGCCCTTTGATTGGATGGCCATTCGGTGTCTTCCTCATGAAACAGTTCAGTGA  
AAATATCCCTACAGAGTTGCTTGAATCAGCTAAAATCGACGGTTGTGGTGAGATTTCGTAC  
CTTCTGGAGTGTAGCCTTCCCGATTGTGAAACCAGGGTTTGCAGCCCTTGCAATCTTTAC  
CTTCATCAATACTTGGAATGACTACTTCATGCAGTTGGTAATGTTGACTTCACGTAACAA  
TTTGACCATCTCACTTGGGGTTGCGACCATGCAGGCTGAAATGGCAACCAACTATGGTTT  
GATTATGGCAGGAGCTGCCCTTGCTGCTGTTCCAATCGTCACAGTCTTCCTAGTCTTCCA  
AAAATCCTTCACACAGGGTATTACTATGGGAGCGGTCAAAGGATAATACTCTGCGAAAAT  
CGAATGCAAACTACGTCAGCTTCACCTTGCCATACTTAAGTATTGCCTGTGGTTAGCTTC  
CTAGTTTGTCTTCAATTTTCATTGAGGTATAGGAAAATCAATCTATCAAGATACAGAAG  
TATATTTTATAGATTTAGAGAATATAGAAGTTATAAGTGTCTACAAAATGGAGGGTATGC  
AGTTACTTTATGAAGTTTTGTGTCAGACACTTATAAACTTAAGAATGGTTTTAGTTAACTAT  
CAGAAAACGAAGGAAAGAGTATGATTTTTGACGATTTGAAAAACATCACCTTTTACAAAG  
GGATTCATCCCAATTTAGACAAGGCTATCGACTATCTCTACCAACATCGTAAAGATTCAT  
TCGAATTAGGAAAGTATGAGATTGATGGAGATAAAGTCTTCTAGTTGTTTCAGGAAAATG  
TCCTCAATCAAGTTGAGAATAATCAATTTGAACACCATAAGAACTATGCAGATTTGCATT  
TGCTGATAGAAGGGCATGAATATTTCGAG

## ORF Predictions:

ORF #	Start	End	Direction	Length
6	446	751	F	102 aa

[SEQ ID NO: ] 3864624-6 ORF translation from 446-751,  
direction F  
VLMVQLSFKFFGKIKWPSLLPTTLYIAIITTINSFQCFALIQLLTSGGPNYSTSTLMYYL  
YEKAFQLTEYGYANTIGVFLAVMIAIVSFVQFKVLGNDVEY\*

## Blastp and/or MPSearch Result:

## Description;

MULTIPLE SUGAR-BINDING TRANSPORT SYSTEM PERMEASE PROTEIN  
MSMF. - STREPTOCOCCUS MUTANS.

Assembly ID: 3864630

Assembly Length: 1773bp

[SEQ ID NO: ] 3864630 Strep Assembly -- Assembly  
id#3864630

ATCGAATTATATATAAAAATCTTACACATTAGAAAAGGAGGTTTCCCATGTACTTTCCAA  
CATCCTCTGCCTTGATTGAATTTCTCATCTTGGCCGTACTGGAGCAGGGTGATTCTTATG  
GTTATGAGATTAGCCAAACCATTAAGCTAATCGCTAATATCAAAGAATCCACACTCTATC  
CCATTCTCAAAAAATTGGAAGGCAATAGCTTTCTGACAACCTATTCTAGAGAGTTCCAAG  
GTCGCATGCGCAAATACTACTCCTTGACAAACGGTGGTATAGAGCAGCTCTTGACCCTAA  
AAGATGAATGGGCACTCTATACAGACACCATCAATGGCATCATAGAAGGGAGTATCCGCC  
ATGACAAGAACTGAATACCTGACTCAGCTAGAACTCTATCTCAAGAACTACCTGAAGCT  
GACCGTATCGAAGCCATGGACTATTTTCAGAGAGCTCTTTGACGATGCTGGAGTCGAAGGA  
GAAGAAGAACTCATCGCTAGTTTGGGAACTCCCAAAGAAGCGGCCACGAAGTTCTATCCA  
ATCTTCTCGATAAAAAAATCAATGAAGCACCCGCTCAAAAAAATAACCGACAAATTTTAC  
ATATCGCCTTGTTAGCCCTCCTTGCAGCACCTATCGGCATTCTCTGGGAATCGCCATCC  
TCGTGACCCTGTTTCGCAATCCTTGTAGCCGCTTTGACTGTCATTCTGGCTTTCTTTGCAG  
TTTCCATACTGGGTATCATCGGCGGATTCTATTTTTAGTTGAAAGTTTCACTATCCTCG  
CCCAAGCCAAATCAGCCTTTATCTTGATTTTTGGTTCTGGTTTACTGGCTATCGGTGCTT

CTTCGCTAGTTTTACTTTGGCATTTCCTATGTAGCTCGCTTCTTCGGTCTACTCATTGTTTC  
 GTCTGGTACAATTTGTTCTTAAAAAAGGAAAGAGAGGTAATCAGCATGCGTAAATGGACA  
 AAAGGATTTCTCATCTTTGGTGTGGTGACTACCGTTATCGGCTTTATCCTGCTTTTTGTA  
 GGTATCCAATCTGACGGGATTAAGAGTCTACTTTCCATGTCCAAAGAACCTGTCTATGAT  
 AGCCGTACGGAAAAGCTAACCTTTGGCAAGGAAGTCGAAAACCTAGAAATTACTCTCCAC  
 CAACACACGCTCACCATCACAGACTCTTTCGATGATCAAATCCACATTTCTTACCATCCA  
 TCTCTTTCTGCTCACCATGATTTTATCACCAATCAGAACGATAGAACTCTGAGTCTCACT  
 GATAAGAAACTGTCTGAAACTCCGTTTCTCTCTTCTGGAATTGGTGGGATTCTTCATATC  
 GCAAGTAGCTACTCTAGTCGTTTTGAAGAAGTTATTCTCCGACTACCAAAGGGGAGAACT  
 CTAAGAGGGATCAACATCTCAGCCAATCGCGGACAAACCACCATCATAAATGCTAGCCTT  
 GAAAATGCGACCCTCAATACAAACAGCTATATCCTCCGAATTGAAGGAAGTCGTATCAAA  
 AACAGTAAACTCACACGCCCAATATCGTTAATATCTTTGATACAGTTCTTACAGATAGT  
 CAGCTAGAGTCAACAGATAATCACTTCCACGCTGAAAATATCCAAGTCCATGGTAAGGTT  
 GAACTGACTGCCAAAGATTATCTCAGAATCATCCTAGACCAGAAAGAAAGCCAACGAATT  
 AACTGGGACATCTCAAGTAACTACGGTTCTATCTTCCAATTCACAAGAGAAAAGCCTGAA  
 TCAAGAGGTACGGAATTAAGCAACCCTTACAAA

## ORF Predictions:

ORF #	Start	End	Direction	Length
8	663	953	F	97 aa

[SEQ ID NO: ] 3864630-8 ORF translation from 663-953,  
 direction F  
 VTLFAILVAALTVILAFFAVSILGIIGGFLFLVESFTILAQAQSAFILIFGSGLLAIGAS  
 SLVLLGISYVARFFGLLIVRLVQFVLKKGKRGNQHA\*

## Blastp and/or MPSearch Result:

Description:  
 unknown

Assembly ID: 3864654  
 Assembly Length: 2307bp

[SEQ ID NO:       ]     3864654 Strep Assembly -- Assembly  
id#3864654

CCACCTTGGATGTTTCTAAACGTTTCGCAAGAATTAGAAGAACAGTTAGCGAAAAATAGAG  
CCTTGGAAGAGACGTTTACTGAGTCGACTCGAATTTCAAAGTAGAAGCGCAGAAGAAGG  
AAAAAGAACGTTTGTAGAGGAATTGACCTTCTTGCAGGAATATATAGATGTAGGTCAAG  
CGAGAGTTCCTTTAGCGGCTACTTTGAGTTTGGAATTTGGTACTACCTCTGTCAATATAT  
ATGCTGGTATGGATGATGATTTTAAACGTTACAATGCACCAATTTTAACATGGTATGAAA  
CGGCTCGCTATGCCTTTGAGCGAGGTATGGTCTGGCAAAATTTAGGTGGTGTGAAACT  
CTCTCAATGGTGGACTTTATCATTTTAAGGAAAAATTTAATCCAACGATTGAAGAATACT  
TGGGTGAATTTACAATGCCCACTCATCCTCTCTATCCTCTGTAAAGACTTGCTCTTGATT  
TCCGTAAAACATTAAGAAAAAACATAGAAAGTAAGTATATGGCACTAACAACACTCAGG  
AAAGAAGAGTTTCAGACTTATTCTGATCAGGTTTCTTCTCGTTTCCTTTATGCAATCTGTC  
CAGATGGGGGATTGCTAGAAAAAGAGGGGCTCGAATTGTTTATCTTGCTTTGAAACAA  
GAAGGAGAAATTCAAGTTGCAGCTCTGGTTTATAGCTTGCCCATGGCTGGGTGGTCTGCA  
TATGGAACCTCAATTCGGGGCCGATTTATACCCAACAAGATGCTCTTCCAGTTTTTTATGC  
AGAGTTAAAAGAATATGCCAAGCAAAATGGTGTATTAGAGTTGCTTGTAACCTTATGA  
AACTTATCAAACCTTTTGATAGCCAAGGTAATCCAATAGATGCTGAGAAAAAAGTATTAT  
TCAAGGTTTGACTGATTTAGGTTATCAATTTGATGGCTTAACAACAGGTTACCCAGGTGG  
AGAACCAGATTGGTTATACTATAAAGATTTAACTGAATTAAGTGAAGAGTTTGCTTAA  
AAGTTTTAGCAAAAAGGGTAAACCTTGGTGAAAAAGGCTGAAACCTTTGGCATTTCGGTT  
GAAAAAGTTAAACGTGAAGAACTATCGATTTTTAAGAAATATAACAAAAGAAACCTCTGA  
ACGTAGAGAATATAGTGATAAAAGTTTAGAATATTATGAGCATTTTTATGATACTTTTGG  
AGAACAAGCGGAGTTTCTCATAGCAAGCTTGAATTTTTTCGGAGTATATGAGCAAATTGCA  
AGGTGAACAAAGTAACTAGAAAGAACTTGGACAAGTTGCGACTTGATTTGAGTAAAAA  
TCCTCATTTCTGAGAAAAAACAAATCAACTGAGAGAATATTCTAGTCAATTTGAAACGTT  
TGAAGTTCGAAAAGCAGAAGCGCGAGACTTGATTGAAAACGATATGGAGAAGAAGATATT  
GTTTTAGCTGGGAGTTTATTTGTTTATATGCCTCAGGAAACGACTTATCTCTTTAGTGGT  
TCCTACACTGAGTTTAATAAGTGCTATGCCCCCTGCACTGCTTCAAAAATATGTTATGTTG  
GAAAGCATAAAACGTGGAATACCTAAATACAATTTCCCTAGGCATTCAAGGGATTTTTGAT  
GGAAGTGATGGTGTTTTGCGTTTTAAACAGAATTTTAATGGCTATATTGTACGCAAAGCG  
GGTACTTTCCGTTACCATCCATCGCCTTTAAAATACAAAGCTATCCAGTTACTCAAAAAA  
ATAGTAGGACGTTAAGATGAAAAAGTCAGTATTTAGATTTCTTTTAGCTTCTTTTAGTAA  
AATCGAATTTTTTATTTGCTAGAAAGGTGGAGAGACATGCGCTGGCTTTTTCGTTTGATAG  
GGGCTTTCTTTTTTTTTGTGTGGCGTTTGTTTTGGCGTCTGGTTTGGATAGTTGTGCTCT  
TATGTGTGCTTGCTTTCGGACTTCTCTGGTATTTGAACGGGGATTTTCAAGGAGCGCTAA  
AGCAAGCAGAACGGTCAGTAAAAATTGGTCAACAAAGTATTGACCAATGGGAGAAAACAG  
GGCAACTGCCTAAGTTAAGCCAGACAGATAGTCACCAGCATTTCTGAAGGAAGGTGGCCAC  
AGGCCTCTGCTCGTATTTACCTGGATCCGCAGATGGATTCACGCTTTCAAGAGGCTTATT  
TAGAAGCAATCCAGAAGTGAATCAAACCTGGTGCTTTTAACTTTGAACTCGTGACTGAAT  
CTAGTAAGGCGGATATTACGGCTACGGAGATAACGACGGAAGCACTCCTGTGGCAGGAGA  
AGCGGAAAGTCAAACCTAATCTCTTAAC

## ORF Predictions:

ORF #	Start	End	Direction	Length
9	1878	2306	F	143 aa

[SEQ ID NO: ] 3864654-9 ORF translation from 1878-2306,  
direction F

VWRLFWRVLVWIVVLLCVLAFGLLWYLNQDFQGALKQAERSVKIGQQSIDQWEKTGQLPKL  
SQTDSHQHSEGRWPQASARIYLDPMDSRFQEAYLEAIQWNQGTGAFNFELVTESSKADI  
TATEITTEALLWQEKRVKLIS\*

## Blastp and/or MPSearch Result:

## Description:

unknown

Assembly ID: 3864658

Assembly Length: 1236bp

[SEQ ID NO: ] 3864658 Strep Assembly -- Assembly  
id#3864658

TTCCCATATATTCCTGTNCTTCACCAGAATTGAGATAAATGATTGTATTTCTCATTTAA  
TGATTGTTCAAATTTGTGAAAGATAGCTTCTTTTGGACGTAACCTCTCCAATTGTTTATT  
TAAAGAGCTCGCTTGTAACCTTCTTGTCCACTTGATAACGAAATAATGACATCTCCAGC  
ATTTACCATATCTCCTTCTGACTTATGTAAAGTAACTACCTTCCCTGAACCAATTGCTGA  
TAGGAACTCTGTACCTGTTATAACTGAATTTCCATTCGCTTTTACAATATAGTTTTTGGG  
TATATAAGCTGCGCCAACCAATGCACCGCTTAAGATAATAGCAGTTGAAATAATGAGAAT  
AAACGCAAAAGCTGGTGGTCTCTTATCAAAGAAAATACGAGAATAACGTAATTCTGATTT  
ATTATATAATTTCATAGGCTTACAATTGGTCTAAAAATATCTACTACCATTTTTTCAGGA  
GAAGAATTAACATAAACTGTATAGACAATCCCATCCGTTTGAATATCATTTTTCATAGACA  
TATAGATCCAATTTAGAATACGCATACTGTAGATACTCTGGACTGTCTTCAAACGAACA  
TATAACAATATGGAACAGAGATAGAATCCTGTACATCATAAATGTTACTGTACTGTTGA  
GCATTATGAGCTTGAATATAAACTCAAATCAGTCGTTATTAATCCATCATCATGAATA  
GTAGTACCACAACCTTTTACAATTAATGGACCAAAAATTTGTGCTTTTAACAACTGCAAA  
TGTTGATGAAATTTATTAATTTCCCTAATCAACATCTTCTACTTTNGTATCATGTAACCTT  
TTACAGATAACTGACTTTTAGTACCAGTTTTTTTATTATCTTTTACCTCTAACTTAGCCATA

AGTAACCTCCTCTGTATCTAACACAGCCTGTGACTGAATTTGTTGATTCACCTTGAACGCT  
CTGCAAACCAACCATTCTAGCATACTTTCCATTTTTTCGCCATTAGTTCTTCATGAGTCCC  
ATATTCCACAATAGTCCCATTTTTCTAAAAAGCATATCTTATCACATCGAAGAATTGTAGA  
CAGCCTGTGGGCTACTACAATTGTTGTCTTATCCATTATTTTATTAAAGATTAAATCCTG  
AATAATCTGTTCACTAAATGAATCTAAGTTAGAGGTTGCCTCATCAAATATATACAAATC  
AGCTTTACTCAGTAGTGCTCTTGCAATAGCCAATCG

## ORF Predictions:

ORF #	Start	End	Direction	Length
7	892	1029	R	46 aa

[SEQ ID NO: ] 3864658-7 ORF translation from 892-1029,  
direction R

VEYGTHEELMAKNGKYARMVGLQSVQVNQQIQSQAVLDTEEVTYG\*

## Blastp and/or MPSearch Result:

## Description:

unknown

Assembly ID: 3864664

Assembly Length: 2124bp

[SEQ ID NO: ] 3864664 Strep Assembly -- Assembly  
id#3864664

CCTCGTTATGCAGATGAACGTTATTTCTTGTCAAAGAGTCACAAGAATTTTGTTGATCGT  
AATCTTTTATTACCATTTCGTGACAAGGAAACCACCTGTATCAAGCCTTATCAGCAGGAT  
TTGGATTTGCCACATGGTCTGGCCTTGGATGTTTTGCCTTTGGATTATTATCCGAAAAAT  
CCAGCTGAGCGGAAAAACNGGTTTCGTTGAGCCTTGATTTATTTACTCTTTTGTGCGCAA  
ACTATTCCAGAAAAGCATGGTGCTCTCATGAAATGGGGAAGTCGCATTTTACTGGGTTTG  
ACTCCAAAATCTCTCCGTTATCGCATCTGGAAAAAGCTGAGAAAGAAATGACTAAGTAT  
GATTTGGCTGATTGTGATGGCATTACAGAATTATGCTCAGGTCCTGGCTACATGAGAAAC  
AAGTACCCAATCACATCTTTTGAAGACAATCTTTTCTTGCCATTTGAAGGAACAGAGATG  
CCTATTCCAATCGGCTATGATGTCTATCTCAGAACTGCTTTTGGGGATTATATGACGCCT

CCACCAGCAGACAAGCAGGTACCGCATCAGGATGCTGTCATCGCTGATATGGATAAGTCT  
TATACAGAATACAAGGGAGAATATGGTGGCTAAGAAAAAATCTTATTTTTTATGTGGTC  
TTTTTCTCTTGGAGGTGGTGCAGAGAAGATTCTATCAACCATTGTTTCAAATCTGGATCC  
AGAAAAGTATGATATTGATATTCCTTGAAATGGAGCACTTTGACAAGGGATATGAATCTG  
TTCCAAAGCATGTACGCATTTTAAAATCCCTTCAAGATTATCGCCAAACCAGATGGTTAC  
GAGCTTTTTTGTGGAGAATGAGAATTTATTTTCCAAGACTGACTCGTCGTTTGCTTGTA  
AAGATGATTATGATGTTGAAGTTTCTTTTACCATTATGAATCCACCCTGTTGTTCTCTA  
AAAGAAGAGAAGTCAAGAAGATATCTTGGATTTCATGGAAGTATTGAAGAACTTCTTAAGG  
ATAGCTCTAAAAGAGAATCACATAGAAGCCAGTTGGATGCTGCGAATACAATTGTAGGGA  
TTTCAAAAAGACCAGCAATTCTATCAAGGAAGTTTATCCAGATTATGCTTCTAAATTAC  
AGACAATCTACAATGGATATGATTTTCAGACTATTCTAGAAAAATCTCAAGAGAAGATCG  
ATATCGAGATTGCTCCTCAAAGTATCTGTACTATCGGACGGATTGAGGAAAATAAGGGTT  
CTGACCGTGTAGTGGAAGTGATACGATTATTACACCAAGAGGGAAAAAATCATCTCTCT  
ATTTTATCGGGGCTGGTGATATGGAAGAGGAACTGAAAAACGAGTCAAAGAGTATGAGA  
TTGAGGACTATGTACATTTTCTTGGTTATCAAAAAATCCTTATCAGTATTTATCTCAGA  
CGAAAGTTCTCTTGTCTATGTCTAAACAAGAAGGCTTTTCTGGAGTGTATGTGGAGGCCT  
TGAGTCTGGGACTCCCTTTTATCTCTACGGACGTTGGAGGGGCTGAGGAATTATCCCAAG  
AAGGACGATTTGGACAAATCATTGAGAGCAATCAAGAGGCAGCTCAGGCGATTACTAATT  
ACATGACTTCTGCCTCAAACCTTAAATGTTCGATGAGGCTAGCCAATTCATTCAACAATTTA  
CAATTACAAAACAAATCGAACAAGTAGAAAACTATTAGAGGAGTAGCATGGAACTGCA  
TTAATTAGTGTGATTGTGCCAGTCTATAATGTGGCGCAGTACCTAGAAAAATCGATAGCT  
TCCATTTCAGAAGCAGACCTATCAAAATCTGGAAATTATTCTTGTTGATGATGGTGCAACA  
GATGAAAGTGGTCGCTTGTGTGATTCAATCGCTGAACAAGATGACAGGGTGTGAGTGCTT  
CATAAAAAGAACGAAGGATTGTGCGCAAGCACGAAATGATGGGATGAAGCAGGCTCACGGG  
GATTATCTGATTTTTTATTGACTCCAAATGATTATATCCATCCCAAGAAATGATCCAGACC  
TTATATAACCAATTAATTCCAAGAAGAATGCCGGATGTTCCAAGCTGTGGTGTTCATGAA  
TGTCTCTGCTAATGATAAAACCCC

## ORF Predictions:

ORF #	Start	End	Direction	Length
7	675	1727	F	351 aa

[SEQ ID NO: ] 3864664-7 ORF translation from 675-1727,  
direction F

VVQRRFYQPLFQIWIQKSMILIFLEMEHFDKGYESVPHVIRILKSLQDYRQTRWLRFLW  
RMRIYFPRLTRLLVKDDYDVEVSFTIMNPPLLFSSKRREVKKISWIHGSIEELLKDSSKR  
ESHRSQLDAANTIVGISKTSNSIKEVYPDYASKLQTIYNGYDFQTILEKSQEKIDIEIA  
PQSICTIGRIEENKGSDRVVEVIRLLHQEGKNYHLYFIGAGDMEEELKKRVKEYEIEDYV  
HFLGYQKNPYQYLSQTKVLLSMSKQEGFPGVYVEALSLGLPFISTDVGGAEELSQEGFRFG



QIIIESNQEAQAITNYMTSASNFNVD EASQFIQQFTITKQIEQVEKLLEE\*

Blastp and/or MPSearch Result:

Description:

amsK protein - *Erwinia amylovora*

Assembly ID: 3864700

Assembly Length: 1660bp

[SEQ ID NO: ] 3864700 Strep Assembly -- Assembly  
id#3864700

ATCGAATTAAATCCATAAACAGATTTGGTGATTTGATAGACGACATTGGACAGTTTGCGA  
TCTGGCAAGACAGAATGTTTGGTCAAACGGCTCAACATGGTCTTACGAATAGCCTGAAAG  
ACTTCTGGATTTCCCTGCTGAATATAGGTCCACAATTGGCGTTTTTTTGCCAGATGCTCC  
GCTGTTTCAGATCGGTTGAGCAGGGTACTGGAAATCACCGTCGTGATTTCAATATGATTC  
AGCAGATATTCTCGCATTTTGGGATGACTCACTTGGGACAAATCAAGCTGGTCTACCAAG  
AGTCGATTGACCTTGAGTTGCTGGTCAATGCACCTTAATCATCACTTGCTCATTGACAGAC  
TGGTCCCTCACGCCCAATCAAGTAACGATAGAAATCGACAGGCAGATAGTACATGGTCTTG  
ACCTGCTGAAGGGGCGTAAAGACAAAGAGATTATCGACATAAAAAGTATGTTTCAGGCAGT  
TAGAACTGGCTAGCACGCAACAAATCTGTCCGATAAATCAGCGAGTGCATCATGATATAC  
TGGCCTTTGGAGAAATTTCCGACCTGGTCCCAGCCAAAAATCTGCCGAACAGGCAAGACT  
GACTCGTAACCTCATACTCTTCTTACGAGACTGACCTTCCCTTTTCATAGACAAAATTGGTC  
ACAAAGACATCCATCTCTTGACCCTTGCTCTCAAGTTCCTGCAAGGTTTCAAGAATTTTC  
AAGTAGGCACGAGGATCCACCAGTCATCACTGTCAACTACTTTAAAATAGCGCCCAGAAG  
CCTCTGCCAAGCCGCGATTGACCACACCGCCATGGCCTTTATTTTCCTGATAGATGGCTC  
TAACGATATTAGGATACTTGCTAGCTAAACACTCAGCGATTTCCCTGAGTCTGGTCCTGAG  
ACCCGTCATTGATAATCAAAATCCCAACTTGCTCACCACCAATCACTAGCGACTCCACAC  
AGTAATGAAGATAGGCTGCTGCATTATAGCTAGAAATGGCGATAGACAATAACTTCATAA  
TCTGCTCCTTTAGGGGACTGATTTTTTCTTATACTCTTCGAAAATCTCTTCAAACCGCGT  
CAACGTCGCCTTGCCGTATAGATGTTACTGACTTCGTCAGTTCTATCTGCAACCTCAAAA  
CAGTGTTTTTGAGCAGCCCGCAGCTAGTTTCCTAGTTTGATCTTTGATTTTCATTGAGTAT  
TACTCTCTCTTGTCACCTTCCTTCTATTTTACCATAAAGTCCAGCCTTTGAAGAACTTTTA  
CTAGAAGACAAGGGGCTTCTGTCTCTATTTTGCCATCTTGGGCATCAAAAAGAGGGGTCA  
TCCCTCTTTACGAATTCAATGCTACTAGGGTATCCAAATACTGGTTGTTGATGACTGCCA  
AAATATAGGTATCTGCTTTCAAGAGGTCATCTGGTCCAAATTCACATCCAATGGGGAAT  
TTTCCCTGCTCTCGGAAACCCAAAATATTCAGATTGTATTTGCCACGGAGGTCTAATTTAC  
TCAGACTTTGACCTGCCCAAGACTGAGGAATTTTCATCTCCACGATAGACACATTTTTAT

CCAACTGAAAGACATCAACACTATTATGGAAAAGAATGGTCTGTGCTAGAGACTGCCCCA  
 TTTCATACTCTGGCGAGATAACCGAGTCAGCTCCCATCTT

## ORF Predictions:

ORF #	Start	End	Direction	Length
-----	-----	-----	-----	-----
6	480	740	R	87 aa

[SEQ ID NO: ] 3864700-6 ORF translation from 480-740,  
 direction R  
 VDPRAYLKILETLQELESKGQEMDVFTNFVYEKEGQSRKKSMSYESVLPVRQIFGWDQV  
 GNFSKGQYIMMHS LIYRTDLLRASQF\*

## Blastp and/or MPSearch Result:

Description:  
 unknown

Assembly ID: 3864706  
 Assembly Length: 1306bp

[SEQ ID NO: ] 3864706 Strep Assembly -- Assembly  
 id#3864706  
 CTGATCGAATTTAAAAGAAGCCCACCCTAATCTGCCTACTTCTTACCTCCAACACTTGGT  
 CGTGTCCAACCTTTATCGAGACATTGACCTGGTGGCTCAAAAAGGTCAAGATTTACAGA  
 CCAGGAAGTTGTCCAATTTTATCTAGACCTTCTCATTCTTAAATTTGAATATAGAGTAA  
 AGCTTCAGTTGTCTTATTTCTAGGTTACTGAGTTTTTTATCTTTTCAACAACAAAAGAGG  
 ACCCGCCGATCCTCTTTTTCATACTATAAATCCTTGATTATCAACTATATCTGTTTTAAT  
 CGAAATCTCAAAACAGCACTTTCAAACATCTTTTCCTAGTTAAGTAAATCAGTATTTTGC  
 TTAGCTGCCTTGCTCCATTGATACCAACCACTAGACTGTTAATGAGATAAATTAGATAT  
 TTCCCTTGAATTTGCAGGCTTTCTCCCCACCAGAGATAGATTGAAAAGACATTGGTAGCC  
 GCCCAGAATATCCACTGTTTCACGGTAAACAGCTGTCATGAGGATTGCCCCTACCCCATTG  
 GTTGCATCTGTGATTGAATCACGATAGGGGACGATTGGCACCAATAGACTGATAAATGAA  
 GCCAAAGGCCAACCACCAAGCACACTAATGGAAAGATACTTTGTCCAGCCCTTGCCGTC  
 CAGTTTACGCGCGACAACTCCTGCTTTTCTTAACTGTGCCTGATAAATCCAAA

CTAGAGTCCAATTGGCTGCATGACTGTGAAGTAAAGTGTGTCAGCACCTCACCATAAAA  
 GCCTTTCTGTAGGGCCAAATAAGGTAATAACAGAGTTAATCAAGCCAAAAAGATAATTAC  
 TTGCTCGACCTTCGATACAAGATTACACAGATAATCCCTGTCAAGCTACAAATCATCCC  
 AATCCAGTCAACAATACGATGTTTCGTAAACCAACTCCAGCCAGAGAGGAAAACTTCCTAA  
 AACCAGCAAATAAATCCACTGGGCAAACTACGATGGGCAAAGAGGTCATCCCAGATAGC  
 CTTCATAGTTCCTGAAAATCCTAAATCAGCCATAGCCGCAACCATACGACGGTAACCACC  
 TGACATTTACCTAGGGTTGTTTTGATATTTTCAATTTTCTTTTGCAAATAAGTATGCAT  
 CATTTCTCCTTTTGTTTTTTAAAGAGCCGTGTCTGGATAGACTTTCGGACGCAACGCTCTA  
 TTAGATAATGAACTGCCTATACACAAGATTTCTAACCTTAGTCGACATGAGCTGAAACCT  
 CTTATTTGTTAAGTAGTTCACNAAATATTATACACCTATTTTATGA

## ORF Predictions:

ORF #	Start	End	Direction	Length
6	336	626	R	97 aa

[SEQ ID NO: ] 3864706-6 ORF translation from 336-626,  
 direction R  
 VCFGGWPLASFISLLVPIVPYRDSITDATNGVGQILMTAVYREQWIFWAATNVFSIYLWW  
 GESLQIQGKYLILYINSLVGWYQWSKAAKQNTDLLN\*

## Blastp and/or MPSearch Result:

Description:  
 unknown

Assembly ID: 3864710  
 Assembly Length: 1676bp

[SEQ ID NO: ] 3864710 Strep Assembly -- Assembly  
 id#3864710  
 AAACACGCTTGGCATGGCAGATAAAGCGAGATTTTTTGTTTTTTCTTGGACTTGGCGTCT  
 TCTTTAATTGTCCTAAATTCCATGATTTAATTGTACTAAAAATAATATAAAGTGCTAGT  
 TTTTACGAATAAAGAAGTATGAAAGTAAATTTAGATTATCTCGGTCGTTTATTTACTGAG  
 AATGAATTAACAGAAGAAGAACGTCAGTTGGCGGAGAACTTCCAGCAATGAGAAAGGAG

AAGGGGAAACTTTTCTGTCAACGTTGTAATAGTACTATTCTAGAAGAATGGTATTTGCCC  
 ATCGGTGCTTACTATTGTGCGAGAGTGCTTGCTGATGAAGCGAGTCAGAAGTGATCAAAC  
 TTATACTATTTTCCGCAGGAGGATTTTCCGAAGCAAGATGTTCTCAAATGGCGCAGCCAA  
 TTAACCTCCTTTTCAAGAGAAGGTGTCAGAGGGACTGCTTCAAGCAGTAGACAAGCAAAAC  
 CCAACCTTAGTTCATGCGGTAACAGGAGCTGGAAAGACAGAAATGATTTATCAAGTAGTG  
 GCTAAAGTGATCAATGCGGGTGGTGCAGTGTGTTTGGCTAGTCCTCGCATAGATGTTTGT  
 TTGGAGCTGTACAAGCGCCTGCAACAGGATTTTTCTTGCGGGATAGCTTTGCTACATGGA  
 GAATCGGAACCTTATTTTTCGAACACCACTAGTTGTTGCAACAACCCATCAGTTATTGAAG  
 TTTTATCAAGCTTTTGATTTGCTGATAGTGGATGAAGTAGATGCTTTTCCTTATGTTGAT  
 AATCCCACGCTTTACCACGCTGTCAAGAATAGTGTAAGGAGAATGGATTGAGAATCTTT  
 TTAACAGCGACTTCGACCAATGAGTTAGATAAAAAGGTCGTTTAGGAGAACTAAAAAGA  
 CTGAGTTTACCGAGACGGTTTCCATGGAAATCCGTTGATTATTCCAAAACCAATTTGGTT  
 ATCGGATTTTAATCGCTACTTAGACAAGAATCGTTTGTACCAAAGTTAAAGTCCTATAT  
 TGAGAAGCAGAGAAAGACAGCTTATCCGTTACTCATTTTTGCTTCAGAAATTAAGAAAGG  
 GGAGCAGTTAGAAGAAATCTTACAGGAGCAATTTCCAAATGAGAAAATTGGCTTTGTATC  
 TTCTGTAACAGAGGATCGATTAGAGCAAGTACAAGCTTTTCGAGATGGAGAACTGACAAT  
 ACTTATCAGTACGACAATCTTGGAGCGTGGAGTTACCTTCCCTTGTGTGGATGTTTTCGT  
 AGTAGAGGCCAATCATCGTTTGTTTACCAAGTCTAGTTTGATTGAGATTGGTGGACGAGT  
 TGGACGAAGCATGGATAGACCGACAGGAGATTTGCTTTTCTTCCATGATGGGTAAATGC  
 TTCAATCAAGAAGGCGATTAAGGAAATTCAGATGATGAATAAGGAGGCTGGTCTATGAAG  
 TGCTTGTTATGTGGGCAGACTATGAAGACTGTTTTAACTTTTAGTAGTCTCTTACTTCTG  
 AGGAATGATGACTCTTGTCTTTGTTTCAGACTGTGATTCTACTTTTGAAAGAATTGGGGAA  
 GAGAACTGTCCAAATTGTATGAAAACAGAGTTGTCAACAAAGTGTCAAGATTGTCAACTT  
 TGGTGTAAGAAGGAGTTGAAGTCAGTCATAGAGCGATTTTTACTTACAATCAAGA

## ORF Predictions:

ORF #	Start	End	Direction	Length
6	442	972	F	177 aa
7	1247	1438	F	64 aa

[SEQ ID NO: ] 3864710-6 ORF translation from 442-972,  
 direction F  
 VSEGLLQAVDKQNPTLVHAVTGAGKTEMIYQVVAKVINAGGAVCLASPRIDVCLELYKRL  
 QQDFSCGIALLLHGESEPYFRTPLVVATTHQLLKIFYQAFDLLIVDEVDAFPYVDNPTLYHA  
 VKNSVKENGLRIFLTATSTNELDKKVRLLGELKRLSLPRRFPWKSVDYSKTNLVIGF\*

Blastp and/or MPSearch Result:

## Description:

COMF OPERON PROTEIN 1. - BACILLUS SUBTILIS.

[SEQ ID NO: ] 3864710-7 ORF translation from 1247-1438,  
direction F  
VDVFVVEANHRLFTKSSLIQIGGRVGRSMDRPTGDLLFFHDGLNASIKKAIKEIQMMNKE  
AGL\*

## Blastp and/or MPSearch Result:

## Description:

COMF OPERON PROTEIN 1. - BACILLUS SUBTILIS.

Assembly ID: 3864724

Assembly Length: 2159bp

[SEQ ID NO: ] 3864724 Strep Assembly -- Assembly  
id#3864724

CTGCTCTCACCATGCGATACGAACAGCATAGGTTTCAACTTTATCAAAGCTAAAGTGGTT  
CAATTCTCCACCCTTGAGTTGAGCAGGGGGCTTTTATAGATTAGTAAGTTGGTTTCCCAG  
TTGGCAGAATCATTAAGACATGGTCCTTACATACCAACAAAGCTAGGGTTTATAGGAGC  
TGTTGGGACAGTCTTACCAACATAATACTCAATCACATAAGACTTCGGTGCACCAACTCC  
ATGGTCTTCATGGAAGCCAACGCTTAAGTTATCAACTGAACGTTTGCTCAAAATACCTGA  
ATCTCCGAATAGGACACCGACTGAAGCTTCTGGATTACTACGATTCCAGTTTGTCCAACG  
ATTGGCTGGTTGGTTATTGTAGGAAATGAGCTTGTCATTAACATTTGAAACTGGGTCGCT  
TGGATTTGAATCTGAAGCAAAGGCAAGTGGCAATTCTGAACCGGTCCATTGGTCAGAAAT  
GTTTGCACCTTGCTCAGTTTGAGCAGATACGCGAACATGAAGTTTAGTTGTTAATTGAGT  
ACCTTCTAAGCGACCATTAACTGTAAAGACACCTTCCTTAGCGTATTGCTCTGGACGAAT  
CGCATCCCATGCAACCTTAGCTGATGAAACGTGACCATTGGAATCATATGTCCGAACACT  
TTCTGGTAATTGTGGTGCTTCTGCGATTGGAGTTGTCACACTGACTTCTTCAACTGAAAC  
GATACCTTCTACAGAGACTTTTGCACGCGCTTCAAGGTCAATTTCCTTCAACTTTACCTAG  
TACTTCAAATGTCTGATAGGAGTCTAGTTTTTCTTTTCGGAATAGCTTGCCAAGTGACTTT  
ATGAGTTTTAGGGAAACCTTTGTCATACTCAACTGTTACTGTTGCTGGAAGACTTGGTTC  
CTGATGCAAATCTGTCACTACATTTACAGGACGGATGGATTGCGCAATCTTCTTCTCAGT  
ATTGGCTTGGATAGTGAGTTCAACTTGGCCTTTAGCTCCCTCATATTCAGCGTTCAAAGT  
GACTGCTCCTGGCTTATGCAACTCAAGCATTCCTTTACGAATTGCGACTTCCCCTTCACC  
ACTTGTAGAGAAGGTTACTTTATCAGCTGGTAATACAGCTTGCGTTCCATCTTGATAGTG

AGCTCGAACCGACAATTTGACAGTTTGGTCTTCTTTGAGACTGTCAGCTTTTTTCCACTTG  
 CAAGCTCAAGTGAGCAATTTTTGGCGCTTCTTCAAGGAATTGAATTGCATAGGTTGAAGA  
 GGGCCACCATCTTTAGGCTGAATAAAGATGCTCGCACGCATGCCGTTTGCTGCGCTTGCT  
 TGAAGAACTGTAACAGCTGCATTTTTAGCACTTGCTGTGACTTCTGGCAACTTAGCTCCA  
 TAAGCAAGAGTGCGGTATTGCATTGGTTTTTGACTAGTAAGACCTGTGACAGCTTCACCA  
 CCAACCGTTACAGTTGGTACTGCAGGTGCCGAGGATTGCCTTCTTCTACCACAAGGGTT  
 GCATGAATTGGTTGACCTTCTAAATAACCGGTGCGTTGAATACGAGAACCTGGAATTGCT  
 AACTTAGCTTTATCTTCTTCGGCAATCTCCCACTTGTCCTCACTTCATACTCTTCAACACTT  
 CCATCAGTCAAAACATAGGAAACAGATTTGTCTACAGAATTCAAGTCAGTATTTGGAGCA  
 ATACGTTTCACAACTGGTAGCTCTGATTTAAGAGCAATCACTTCTACACGAGCTTCTACT  
 TCTCGTCCGTCAGCCATACCTTTCACCGTTACAATACCAGGCTTGCTCACATCTACTGAA  
 GACCAGGTTACAGGACGTTCTGCACGGCTACCATCACTGTATACAAACGGAACAGTGGA  
 GGCATTTTCAGGTGCCTCTCCAATAATGGTCTGTACTTTTGGCACTTCTGTCCCCAAAACA  
 GTCTTCTCTTGTCTTCTTTCTTACCAGTAAAGACAGTGACTTGGTTTCGATTTCAAGAGA  
 TCAGAGTGGGCAGTAAGGGTGAATTTCCCTGCTTGTTTCAGTTGATTTGACAATGGCAACA  
 CCTTTACCATTAAATGCTTTACGAATCCAAGAACCATCTGCTTGCGCCTTATAGCGTTCA  
 CGACTGGCTTGTTCTCCGTTATCTACACCGACCAGTTGACCTTGGCCATGCAATTTCGAT

ORF Predictions:

ORF #	Start	End	Direction	Length
6	133	1197	R	355 aa

[SEQ ID NO: ] 3864724-6 ORF translation from 133-1197,  
 direction R  
 VEKADSLKEDQTVKLSVRAHYQDGTQAVLPADKVTFSTSGEGEVAIRKGMLELHKPGAVT  
 LNAEYEGAKGQVELTIQANTEKKIAQSIRPVNVVTDLHQEPSLPATVTVEYDKGFPKTHK  
 VTWQAIPKEKLDSYQTFEVLGKVEGIDLEARAKVSVEGIVSVEEVSVTTPIAEAPQLPES  
 VRTYDSNGHVSSAKVAWDAIRPEQYAKEGVFTVNGRLEGTQLTTLKLVHRVSAQTEQGANI  
 SDQWTGSELPLAFASDSNPSPVSNVNDKLISYNNQPANRWTNWNRSNPEASVGVLFGDS  
 GILSKRSVDNLSVGFHEDHGVGAPKSYVIEYYVGKTVPTAPKNPSFVGNEGPCPCL\*

Blastp and/or MPSearch Result:

Description:  
 unknown

Assembly ID: 3864734  
Assembly Length: 2199bp

[SEQ ID NO: ] 3864734 Strep Assembly -- Assembly  
id#3864734

CTTATCGTACTAAGGATGGCAGTGTTCAACTGTTCCGTCCTGATGAAAATGCTAAACGCC  
TGCAACGTACATGTGACCGTCTCTTGATGCCAACAAGTTCCGAACAGACATGTTTGTAGA  
AGCTTGTAAGCAGTTGTCCGTGCGAATGAAGAATACGTACCACCATACGGAATAGGTGG  
AACTTTATATCTTCGCCCTCTTTTGATTGGTGTCGGAGATATTATCGGGGTAAAACCGGC  
AGAAGAGTACATTTTCACCATCTTTGCTATGCCAGTTGGAAATTACTTTAAAGGTGGTTT  
GGTCCCAACCAACTTCTTGATTCAAGGATGAGTACGACCGTGCAGCACCAATGGTACAGG  
TGCGGCTAAGGTTGGTGGAACTATGCTGCAAGTCTCTTACCAGGAAAAATGGCCAAGTC  
ACGCCATTTCTCAGATGTTATCTATCTGGACCCATCAACTCATACAAAGATTGAAGAAGT  
CGGATCAGCTAATTTCTTTGGAATTACAGCTGATAATGAATTTGTAACACCATTGAGTCC  
ATCTATCTTGCCATCTATTACCAAGTATTCCTTGCTTTATTTGGCAGAACATCGCTTGGG  
ATTAATCCTATTGAGGGTGATGTTCCAATTGATAATCTTGACCGTTTTGTAGAGGCAGG  
TGCTGTGGTACAGCAGCGGTTATTTCTCCAATTGGAGGTATTCAACATGGTGATGATTT  
CCATGTATTCTATAGTGAAACAGAAGTAGGTCTGTGACGCGTAAATTATATAATGAATT  
GACGGGTATTCAAGTTTGGCGATATTGAAGCGCCAGAAGGTTGGATTGTAAAAGTAGATTA  
AAATAAACCAAGGAGATTTTTTATGAAATAGAAAAAGTGGCTCTTAACAGCAGGAGTGG  
TCCTGAGCACGTCAGCTATTTTAGTGGCTTGTGGAAAACTGATAAAGAACCAGATGCAC  
CGACAACATTTCTTATGTCTATGCAGTAGATCCAGCATCATTGGGCTACAGTATACCGA  
CTCGAACATCGAGGACAGACGTTATTGGAATGTTATTGATGGTTTGATGGAAAATGATA  
AATACGGCAATGTTGCTCCTTCTCAAAAAGACTATGATTGTAACAGTACAGGATGGGCTC  
CAAGCTATCAAGATCCAGCGTCTTACTTGAATATTATGGATCCAAAATCTGGTTCTGCCA  
TGAAACACCTTGGCATTACGAAAGGAAAAGATAAGGATGTTGTAGCTAAACCTGGTTTGG  
ATAAATATAAGAAATTGTTAGAAGATGCTGTTTCTGAGACCACTGACCTAGAGAAGAGAT  
ATGAAAAATATGCCAAAGCTCAAGCTTGGTCGACAGATACTTCATTATTGATGCCAACAG  
CTTCATCTGGTGGTTCTCCAGTTGTAAGTAACGTACTACCATTCTCAAACCATACCTCAC  
AAGTTGGTATTAAGGGGAACCATATATCTTTAAAGGAATGAAATTGCAAAAAGATATTG  
TTACAACAAAAGAATATAACGAGGTTTTTAAAAAATGGCAAAAAGAAAAATTGGAATCCA  
ATAGCAAATACCAAAAAGAACTAGAAAAATCCATTAAATAAGGAATGGTATTGATCTTGA  
TAAAATTTTCAAATACTGTCATTTTGAATATAAAGGAGTTTGATATGGAGTGGATTACA  
TTAATAGGAATAGCAATCATTGTTGTGGGTCTTATTTACAAATTTGATACAATTGCAAC  
AGTAGTCTTAGCTGGTTTGGTTACAGCTTTAGTTTCAGGTGTTTCTCTCGTTGAATTTTT  
GGAGATTTTGGGAAAAGAATTTAGCAATCAGCGAGTGCTCACGATTTTTTATGGTTACCTT  
GCCTCTTGTGGGGCTGTCAGAAACCTTTGGACTCAAGCAACGATCAATCGATTTGATTCTG  
AAAGATTAAGGTCTGACAGTTGGAACTTCTATACAGTTTATTTCTTTATTCGAGAGTT  
AGCTGGTTTCTTTTCAATTCGTCTAGGAGGACACCCTCAGTTTGTGACACCTTTGGTTCA  
ACCTATGGGAGAAGCAGCTGCAGAGTCTCAATTAGGTAGAAAGTTAACAGAGGTTGAAGA  
TGAGACAATAAAAGCGCGTGCGGCTGCGAATGAAAATTTTGGAAATTTCTTTGCTCAAAA

TACGTTTGTAGGTGCTGGGGGAGTCCTCTTGATAGGGG

ORF Predictions:

ORF #	Start	End	Direction	Length
7	897	1601	F	235 aa

[SEQ ID NO: ] 3864734-7 ORF translation from 897-1601, direction F

VVLSTSAILVACGKTDKEPDAPTTFPYVYAVDPASLGYSIPTRTSRTDVIGNVIDGLMEN  
DKYGNVAPSQKDYDLNSTGWAPSYQDPASYLNIMDPKSGSAMKHLGITKGKDKDVVAKPG  
LDKYKKLLEDAVSETTDLEKRYEKYAKAQAWSTDTSLLMPTASSGGSPVVS NVLPFSKPY  
SQVGIKGEPYIFKGMKLQKDIVTTKEYNEVFKKWQKEKLESNSKYQKELEKSIK\*

Blastp and/or MPSearch Result:

Description:

aliB protein - Streptococcus pneumoniae (oligopeptide binding protein)

Assembly ID: 3864740

Assembly Length: 1118bp

[SEQ ID NO: ] 3864740 Strep Assembly -- Assembly id#3864740

CTCCTATTGGTATTTTGCAGAAATTTTCTCCATCAATCCAGTCTGGATAAAGACCAATAG  
TCCAAACCCAAAAAGTAGGAAGACTGAGCCACCTAAGAGTAGACTGAAGGCGGACAGATA  
AAGAACCATCACAATGAGGACAAGAATGGCTAACATGAGGAAGAACCAAGGAAAGTTAAA  
ACTAGCCAACATCAATCCTTTTTGAAGAATTTCTTTCCAAGATAGGTCATAACGTGCCGC  
GATAGGGTAAC TAGCCAGCATCACGATAGTAAGAAAAATCAGAATACCTAAACAAATGGC  
TTTCAGCAATTGGAAGGGCAGAGCTGTTTGACCCAGAAAAGATAGAGATCTGAAAGGGT  
AAGAAACACAATTCCTAACTCCATTAAACCCAGCTGAAGACCTAGTTTCAGATTTTGCTT  
GAAAGATCTTAGATAGATTTTAAAAACAGGCACCCGTCTGCTCTTCTTAACTTCGAACAT  
GGTCTCGTAGAGGCTGATTTTAGCCACTCCAATCGTCACGATGGGTAAACAAGAGACGAC  
AAAAAGAAGATTGGCTGTCACGATGTCCAAGACCTTCTCACTAAAACGCATGAGAAAGTT



ATCTGTATCAAATGCTGCCTTGATAAGGCTTACTCCTTTTTGTGCCATGTTTGCTCCTCC  
 ATCATTTTTCTTTGTAACTGTTTTCTTTTTTGTGTCAGTAAAGCTTTCATAAGTCCCTACC  
 ATGAACAAATCTATTTTTCTTTTTCTTTTGGACTTTTTCTATTTTTATCTATGGATAT  
 ATAATGTATATATAGCGAGGACAACGCACTAGCTAAAATATTACGCCAAGTGTGTTTCATC  
 AAATCCATTTATTCTCCACGGATTATCATTGCAAGCACTGTCCAAGCTAACATATACAA  
 TAAAAAATACAAAGTGCTTTCATTCTCGCATTTTAAAAGTTTATACGACCATTGTTAGGG  
 ATTTTATCATGTGCATCCCAAGCTGCAGCAATATTGTAGGCAAATTACCATATACATCA  
 GCTACATTACAGCTATTTGTAAAATCCTTCCAGAAATCTTGGTCAGTAATCCTACTCTT  
 GCTGCTGCAGTTGCAGCTGCCCTACTTAAGATCGATCG

## ORF Predictions:

ORF #	Start	End	Direction	Length
-----	-----	-----	-----	-----
6	4	264	R	87 aa

[SEQ ID NO: ] 3864740-6 ORF translation from 4-264,  
 direction R  
 VMLASYPIAARYDLWKEILQKGLMLASFNPWFFLMLAILVLIVMVLYLSAFSLLLGGG  
 VFLLFGFGLLVFIQTGLMEKIFAKYQ\*

## Blastp and/or MPSearch Result:

Description:  
 unknown

Assembly ID: 3864792  
 Assembly Length: 1431bp

[SEQ ID NO: ] 3864792 Strep Assembly -- Assembly  
 id#3864792  
 TCCAAATAAGGAAAATAACACTTCTCAAGAAAAACACAACAAGAAGAAACGCCAAAATC  
 TAGCGTCAAGGAAGAGAAAAAAAATCAGAAAACCAGCAACTTCAGGACTCTAATAACA  
 CCTGCTACAAGTAAACCTGCCACTGAAAATGAAAAACAGCCCAATACTCCAATTTTCAGAA  
 AATAATACTCAATGAAAATCAAAGAGCAAAGTAGGAAGCTAGCCGTAGGCAGTACTTGAG  
 TACGGCAAGGCAAAGCTGACGTGGTTTGAAGAGATTTGCGAAGAGTATAAAAGTAATCAA

TAGCCAGTAAAAATAGCTCCTTCCAACCTTGGAAAGAAGCTATTTTTTTATTGCTGCAATAC  
 TTTTCTTGCTTGGTACCTTCAGCTGGACCAATGACACCTGCCATCTCAAGCTCTTCCAT  
 GAGACGGGTGCGACGGTTAAATCCAACCTGACAAACGACGCTGAATCATGGATGCACTGGC  
 TTTCTGTGTTTCGATAACCAAAGACTTAGCTTCTTCAAAAAGCGGATCACCACCAGCATC  
 TCCATCCGAAAATTCTCCTTCATTTTCAGAAACCTCACCTGGATCAAACTCTCATCGTA  
 GTCTGCATCTGCCTGAGTCTTGATGAAGTTCACAATGCGCTCAACATCGTCATCCGAGAT  
 AAAGGAGCCTTGGAGACGAACTGGATGATTTTCATTAATCGGTTTAAAGAGCATGTCTCC  
 TCGACCAAGAAGTTTTTCTGCTCCATTTTCATCCAAAATCGTACGGGAGTCTGTTCTCTGA  
 TGAAACCGCAAATGCTACACGAGATGGAACATTGGCCTTAATCAAACCAGAGATGACATC  
 AACAGATGGACGCTGAGTTGCAAGAATCATGTGGATACCTGCAGCACGCGCCTTCTGCC  
 AAGACGGATGATAGCATCTTCCACTTCCTTGCTGGCCACCATCATGAGGTCAGCCAACTC  
 ATCCACAATCACGACAATGAATGGTAGCGGAATTTGCTTGTACTCAGACTGGGAATCGAA  
 CTCGTCTACCTTGGCATTAAAACCTGCAACAGCCCGAACTCCCACCTTGGCAAAGAGTTC  
 ATAACGGTTTGCCATTTTCATCCACAACCTTTTGACAGCCCTGCTGGCTTTGCGTGGATT  
 GGTCACCACTGGCAATCTAACAGGTGGGGAATATCACTGTAGAACAGATAACTCAACCAT  
 CTTTGGGATCGACCACCCATCCTCAGTAAATTTAACTTGATCTGGTCTCGCCTTCATGAG  
 AATGCTANCAATAATGCCGTTAACTGCTACTGACTTCCCTGAACCCGTTGAACCTGCAAC  
 TAGCAAGTGGGGCATTTTAAAAAGGTCAAAGCTCTTGCGGTTCCATTAACAGCCTTCCC  
 TAAAGGAATTTCCAAGAAATTTTCTGCTTCGTTTGCGATTGTTCCATAGTT

## ORF Predictions:

ORF #	Start	End	Direction	Length
6	346	1149	R	268 aa

[SEQ ID NO: ] 3864792-6 ORF translation from 346-1149,  
 direction R

VVTNPRKASRAVQKVVDDEMANRYELFAKVGVRVAVAGFNAKVDEFDSQSEYKQIPLPFIVV  
 IVDELADLMMVASKEVEDAIIRLGQKARAAGIHMILATQRPSVDVISGLIKANVPSRVA  
 AVSSGTDSTILDENGAEKLLGRGDMLFKPINENHPVRLQGSFISDDVERIVNFIKTQA  
 DADYDESFDPGEVSENEGEFSGDAGGDPLFEEAKSLVIETQKASASMIQRRLSVGFNRA  
 TRLMEELEMAAGVIGPAEGTKPRKVLQQ\*

Blastp and/or MPSearch Result:

## Description:

STAGE III SPORULATION PROTEIN E. - BACILLUS SUBTILIS.

Assembly ID: 3864830

Assembly Length: 1412bp

[SEQ ID NO: ] 3864830 Strep Assembly -- Assembly  
id#3864830

AGACAATCTGATCAATCCCGTGGGTCGGAACTCCAAAGTATGTGCTTTTATGTTCAAGG  
GATACAGGGCTTGGTAAATCTTCCGTTCGCGGTCAACCCCCATTTTAAAGCCAGAGCTAG  
CAGTCGGGTCATTTGATACAAATTCATAATTCTTCTCTTCATCTTGCCACTGCAGATAGT  
AGGCCTCTTTCCAGCGCCCTTCTTTTAATAAAGTCAGAATTTCTGTCTTTTCGCGTCAAAA  
GATTTTTTTTGCACGTCTAAATTATTTTTCAGCAAAGTGGTATTCCTCCGAGCTGGTATCAG  
ACATTTGGGAGAGTTTCTCTTCATTTTCATTGATGACTCTCTCACGGTCTACAAGACGAG  
TTTCCAAGTCTCTCTCCAAGCTGACTGAGTTTGCAGTCTGACTATTTAAATAAAAGGTAA  
CACCGAGTACAGATGCAAATAAAAGTAAGATAATCCAGTTTAAACGACTTTTGAAAAGTTT  
TTTTCAATAAAAATAGACTAACATCTTTCATAAACTAAACCTCTTCTATCTGCCCCCTGAT  
GAATGGTTACTACTCTATCGCAGATATCAACCAACTCTTCCTTATAGTGGGAACTTAAAA  
GAACCAGCTGTTCTTGTCTATCGATTTGTGCTAGCCTATCAAAAAACTTCTGTCTATAAT  
ACTCGTCTAAGCCATTTGTAATCTCATCCATGAGCCAGCATTTGGCCTGACTGAGAAAAAT  
ACATAGCAATCACCAAGCGTTGCTTCATCCCTAAGGAATACTTGCGGATGGGAAGACTGA  
TATAGTCAGCCATTTCCCAGTAGGCGATTTTCATCTCTCAAGTTTAGGTCTGACTTCCAGA  
TGTTTTTTTATGAGACGAAGGTAGTCCATCCCAGTTAAGTTTCCATCCAGCCATTCAACGC  
TCTCATAATAAAACAAAGAAGGAGGAAGTGCATGTGTCCACTACTAAGGGGAAGCAACT  
TGCTCATAGCTCGGAATAGTGTCTCTTCCCGAGCCATTGATAGCAAGAAGGCCATAAA  
TCCTACCCTTTTTTAAAGGTAAAATCCGCATCTTGCAAGATGACTTGTCGCGTTTTTAAAG  
TAACATGAGTAAGATTTAACATATCCAGCCCTCCTTTTCTCACTCTTTAAGGATTAATAA  
CCTCCAGTATAGTAGTTTATGACCTCATAACGAGCGTAGTTCCAGCCTCCGCCAACTTTA  
TACTCAGAATAGCTGTAATAACGAGACCATTCCGGAATCCAAGCATACTGATGGTCGTGA  
TAGTTGGTACTATATTCCAAAACCGTATTCCAATCATACTTGTAAGTTTATAGTGGCTGTC  
ACAGCAGATACACTGGACTGAAGAATACCAATAGATTATAAACTAACTAATAAAACAACT  
TTTGCTGATTTTTAATGATTTTATATCCTCAA

# ORF Predictions:

ORF #	Start	End	Direction	Length
6	515	1123	R	203 aa
7	1134	1322	R	63 aa

[SEQ ID NO: ] 3864830-6 ORF translation from 515-1123,  
direction R  
VRKGGLDMLNLTHVTLKTRQVILQDADFTFKKGRIYGLLAINGSGKTTLFRAMSKLLPLS  
SGHIAVPPSLFYYESVEWLDGNLSGMDYLRLIKNIWKSDLNLRDEIAYWEMADYISLPIR  
KYSLGMMKQRLVIAMYFLSQAKCWLMDIEITNGLDEYYRQKFFDRLAQIDRQEQLVLLSSHY  
KEELVDICDRVVTIHQQQIEEV\*

Blastp and/or MPSearch Result:

Description:

ATP-BINDING PROTEIN BEXA. - HAEMOPHILUS INFLUENZAE.

[SEQ ID NO: ] 3864830-7 ORF translation from 1134-1322,  
direction R  
VTATKSYKYDWNNTVLEYSTNYHDHQYAWIPEWSRYYSYSEYKVGGGWNRYARYEVINYTYG  
GY\*

Blastp and/or MPSearch Result:

Description:

unknown

Assembly ID: 3864848

Assembly Length: 1640bp

[SEQ ID NO: ] 3864848 Strep Assembly -- Assembly  
id#3864848  
CTAACAAGGTCATGATACCAGCACTAGCCAAGGTAGCATTAGCTTCTGTACCTGTGTTTG  
GCAATTCCTCTCTCTTACCTGTCTCATAAGTCGGAACCTTCTGGGTCTGGATTCACTGGAG  
TTTCAGTTTTTGGAGTACCTGGTTCTGGAGTTGGTTTATCTGGTGTTGATAAACGGTCAT  
ACCTTACCGTTATTTCTTTATCACTAGAGTCTGACGTAACCTTCTGTGATTCAACTGTTG  
GAATATCTGGATCTTTGTACTTGTCAATCTTACCAGATATAACCTCGTCCCAGTTTCCTG  
TTGTCCATTCACCGTAGGTTACAACCTCCCGTGACCTTGTTCCTCAGTTTTTGTACGGCTTA  
AGGTTACAGGTTGAACAACATCTTCTTTTACATTTTGGTTTCGTAACCTTTATCAACGTAAT  
GAATGATACGCGTTATAGTCTTCGTCTCAGTAGAGGTTGCTGTTTTGGGAACCACTGTTT  
CCTCAACATTCTCACGGTAGTAATAGTCAACTGTTGCACCGTCTTCTGGTACGCATTTGC

AGGAGTTGCTACCAAGGTGTATGTTGTTTTCTTGTGATAACTCGGTCCTTCTTTGTCCTC  
 AGTTGTTGTTTTCCCTTCAATAGTTTTTGGATTCTGTGGTATACTCAGAACCTATCGCTAA  
 ATCAGCTTTTATAACAGACTCTGCCAACTTCTCTGGCTACCTTCTTTATAGTAATTCTGA  
 TGTTACTGTAGCAGTGGTTGGCGCTTCGCTTTACTCTATAAACTAAGGTCAGTGTCTAC  
 CTTTCGCTTACAATATTTCCAGTTAACTTGCAGAATTTGTATCTGCTTCTTTAAAAGTAT  
 AATATTTTCCGTCAGTAGTAGTCATGCTACTGAGTTTTTTTATCTGTGACATAATAGCTGG  
 TACCAATCAGTTGTTTTTTATTGGTAATGTAGGTTCCGTCACCTTTCTTTTCTCCAATTC  
 CAGTATCATTTTTTCAATGATAGCAAACGCCCTTGTTTCATCAACATAGCGAACTTTCACAT  
 TTTCTGAGATTAGTTCTGCCAATTCTGAGGTTTTTTTCTTTTCTTGATTTCTTCGGTTA  
 TTTTCCCTTTCTCTTCTTCGGGAATATTTAGTTTTGGAATGATTTTTTCAACAACGGTTC  
 GTGATGGTTCACAGTATCTTGGATGACTGAAAAGTCAGCTAGAATTGGGAGATTATAAT  
 GAACACGGTGACTTTGAGTGTTTACTCCTACTCTTTCATTATTCTCTGAAAATACTCGTA  
 CGGTATAAGAAACAACATCTTTTCCTAATAGAACATCCCCAGTAGAGAAATAGCCGCCTT  
 TTCCTAGTTTGCTATCTCCAGAGTCCACTTCTTTCCTAATCTTATCAGATAGTTTTTTAC  
 CAGTCAGTACATTTCGTTTCGCACAATCCCTTTGTCTACCCCTACAAAGTGGGAGAACTTTT  
 TGAACTCTTCAGAACCAGATCTAGCCCAACCATTATTAAGGGCATTTGCTTTTGTATTTG  
 TATTCTCTCTCAAAGGTTTGGCGATTAGAATTATATTCATCGGCACTTAGAGTTGCTGCT  
 ATATCTGACTCTTGAATACCAACTTCCTTACTACCATTCTAGCGGCAGTATATGTGAAT  
 TAATCTGTTTATACTTCTAG

## ORF Predictions:

ORF #	Start	End	Direction	Length
6	707	1546	R	280 aa

[SEQ ID NO: ] 3864848-6 ORF translation from 707-1546,  
 direction R

VPMNIILIAKPLRENTNTKANALNNGWARGSGSEEFKKFSHFVGVDKGIVRTNVLTGKKLS  
 DKIRKEVDSGDSKLGKGYFSTGDVLLGKDVSYSYTVRVFSENNERVGVNTQSHRVHYNLP  
 ILADFSVIQDTVEPSRTVVEKIIPKLNIPREEKGKITEEIKKKKKTSELAELISENVKVR  
 YVDEQGRLLSLKNDTGIGEKESDGTIYITNKKQLIGTSYYVTDKKLSSMTTDTGKYTFKE  
 ADTNSASLTGNIVSEGRVTVLVYRVKRSANHCYSNIELL\*

## Blastp and/or MPSearch Result:

## Description:

MURAMIDASE-RELEASED PROTEIN PRECURSOR (136 KD SURFACE  
 PROTEIN). - STREPTOCOCCUS SUIS.

Assembly ID: 3864878  
 Assembly Length: 861bp

[SEQ ID NO: ] 3864878 Strep Assembly -- Assembly  
 id#3864878

CTGGGGGAAC TCAAATTGTTAATGTTATCATCAAGGGCGGATGTAACAAGGTTATGTNGG  
 AAGCCTTTCTGCCTCAACTTCAAAAAGATTGAACGTGGAAGGTGTCAAAGTGACTATCGT  
 CCACTCAGCGGTCGGTGCTATCAACGAATCAGATGTGACCCTTGCCGAAGCTTCAAATGC  
 CTTTATCGTTGGTTTCAACGTACGCCCTACACCACAAGCTCGTCAACAAGCAGAAGCTGA  
 CGATGTGGAAATCCGTCTTCACAGCATTATCTACAAGGTTATCGAAGAGATGGAAGAAGC  
 TATGAAAGGGATGCTTGATCCAGAATTTGAAGAAAAAGTTATTGGTGAAGCGGTTATCCG  
 TGAAACCTTCAAGGTGTCTAAAGTCGGAACATCGGTGGATTTATGGTTATCAACGGTAA  
 GGTTGCCCGTGACTCTAAAGTCCGTGTTATCCGTGATGGTGTCTGTTATCTATGATGGCGA  
 ACTCGCAAGCTTGAAACACTACAAAGATGACGTGAAAGAAGTGACAAACGGTCGTGAAGG  
 TGGATTGATGATCGACGGCTACAATGATATTAAGATGGATGATGTGATTGAGGCGTATGT  
 CATGGAAGAAATCAAGAGATAAGATTTTTTGTCTCTTTCTTAGGTGGTGAGGGACGCAAG  
 CAAACCGATGGTTTCATTGCTTATTTTTGAGCCTAGGGTCTCAAAAATCCCCTGTGATGG  
 GACTGATAAATCAGTTCCATCACTTTCACCACGGCGAAAGAAGCAGATGACTTCAAATTG  
 AACTTCGTTTCAATTTAAACTGAAAATCAAGAAGTTTAAATAGCTAGGTCTGCTGGCCT  
 AGCTTTTGGTTCAAAGTAGAG

#### ORF Predictions:

ORF #	Start	End	Direction	Length
6	95	622	F	176 aa

[SEQ ID NO: ] 3864878-6 ORF translation from 95-622,  
 direction F

VEGVKVTIVHSAVGAINESDVTLAEASNAFIVGFNVRPTPQARQQAEADDVEIRLHSIIY  
 KVIEEMEEAMKGM LDPEFEK VIGEAVIRETFK VSKVGTIGGFMVINGKVARDSKVRVIR  
 DGVVIYD GELASLKHYKDDVKEVTNGREGGLMIDGYNDIKMDDVIEAYVMEEIKR\*

Blastp and/or MPSearch Result:

Description:

INITIATION FACTOR IF-2. - ENTEROCOCCUS FAECIUM  
(STREPTOCOCCUS FAECIUM).

Assembly ID: 3864950  
Assembly Length: 1469bp

[SEQ ID NO: ] 3864950 Strep Assembly -- Assembly  
id#3864950

ACTCTTTCAAGGAATAATTGCATATGTTTGAAGACAAATCTCAAACAACTTAGTCCTTTT  
ATTATACTGTAAGAAGATATAGTTTTCAATTATAGTTTTTCTCTAACTAGTTATAGTCTA  
TTTTTATATCCTAGTGTAAGAAAACAGCCCTAGGGACTGTTTTTCATTAATAATGCATAA  
GAACTTTGTAGTCGTAGTCACCAATTTTTTTTACGGCCGTTCAATTCATCCAATTCAACA  
AGGAAGGCACAACCTGCCATAACACCACCAAGTTTTTCAATCATCTCGATAGTTGCCTTA  
ACAGTTCCACCTGTGCGCAAAAGGTCATCTACAATAAGAACACGTTGACCTGGCTTAATG  
GCATCCGGCGTGTCATAGTTCAAGGTATTCGACACCGTACTCTTTTTTCATAGTCAGCAGAA  
ATAACTTCGCGTGGCAATTTACCTGGCTTACGAACAGGCGCAAAACCAATTCCCAACTCA  
AAGGCAACTGGACAACCCACGATAAATCCACGAGCTTCAGGGGGGGTCCCACGGGGGGAT  
CATGCCGACTTTCTGGTCAGTAGCATACGTGAACGATCCCACGGGGGAACAGGAATTCGT  
AGCTATAAGCATTTCATCAGCCATCAAAGGACTAATATCACGGAAGGTAATGCCTTCCT  
TTGGATAATTTTCAATTGTTGCAATGTAATCTTTTAAATTCATCTTTTTCTTTCTTTCAA  
AGTTTTTTTACTCTCTATTATAGCATATTTTTTAAAGAAAGAAAAAGGAAAAGTTAACTTC  
AATAATTATCTAACGTTTTTGACGATTTATAACTAGCCATCGCAATAAAGCCCAATTTCTG  
TTTATTCTTAGCAAACATTTTATACATAGTTAAAACTGCTTTCTATTCTCCTTTTTTACA  
AGCATTTACACAAAATTTCAAAGTTCCTAGCAAACCTTCGTCATAAATCATACCCGATAA  
TTTCATTAATGTCATTTTACCAGTCAATGCTTTTACATCACAATAACCTGATTCTATCAT  
CACCTGTTCCCAACCATCTTGAGTTAAAGGACCTACATTTACATGAATTGCTTGTGATAA  
TTCCTGTCTGATAGACTCTTTAGCTTCCTTAAGAAGCACATCATGTGTCAAGAGAAGACC  
TCCAGGTTTTAATACCCTTAGATATTCCATTACACATTTTTTCTTAGCTTGATCGGCTTG  
CATAGTCAGCATAGCTTCATTTATAACAATATCAAACTAGCATCTTGATAAGGAAGTTT  
CATTGCATTTGCTCTTTTCAAACCTGATTAAATGAGCAACACCTGCCGTTCCAGCAGATTT  
TTTAGCCACTTCTAAAGCTTGAGCATCCATATCAACAGCAGTTATCTTGCAACCAAAACG  
CTGTGCCAACTCAATTGCTGTAGTTCCCCTATTACACGCAACCTCTAGTATTCTCTTTTC  
TTTTGGAAATCCTCCTTCTGCAATTTCGAT

ORF Predictions:

ORF #	Start	End	Direction	Length
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6 198 500 R 101 aa

[SEQ ID NO: ] 3864950-6 ORF translation from 198-500,  
direction R  
VGCPVAFELGIGFAPVRKPGKLPREVISADYEKEYGVEYLELCTPDAIKPGQRV LIVDDL  
LATGGTVKATIEKLEKLGGMAGCAFLVELDELNGREKNW\*

Blastp and/or MPSearch Result:

Description:

ADENINE PHOSPHORIBOSYLTRANSFERASE (EC 2.4.2.7) (APRT). -  
ESCHERICHIA COLI.

Assembly ID: 3864954

Assembly Length: 1073bp

[SEQ ID NO: ] 3864954 Strep Assembly -- Assembly  
id#3864954  
CTAAATAGGGTATAATATGGGTAATCATTTGTCGTAGGTTTTGTCTGAAATATTGTCCAG  
ACAAGGCTCACAGCAGTTAAATCTTCTGAAAAAGTCAGATTTAATAGCTGCTCTTTTTGT  
GCTTTTTTTCAAGATTTTGAGCATTTGTAACAGAGGCTTAAAGATTCTGAAAATTCGTCA  
AGAGGACACGGTGATAAGGGGTTTACAACCATATGGCGATTAGAAAAGCCTGATTGACAA  
GGCTTGGAACCTATTTACAAAGGAGAATCATCTTGGCAGGACATGACGTTCAATACGGGA  
AACATCGTACCCGTCGTAGTTTTTCAAGAATCAAAGAAGTTCTTGACTTACCAAATTTGA  
TTGAAATTCAAACCTGACTCATTCAAAGCTTTCCTAGACCACGGTCTTAAGGAAGTGTTTG  
AAGATGTATTGCCAATTTCAAACCTCACAGACACAATGGAGTTGGAATTTGTTGGATATG  
AAATCAAGGAACCAAATAACACGCTAGAAGAAGCTCGTATCCACGATGCTAGCTACTCAG  
CACCAATTTTTGTAAACCTTCGCTTGATCAATAAAGAAACAGGCGAAATCAAGACCCAAG  
AAGTTTTCTTTGGTGATTTCCCAATCATGACAGAAATGGGTACTTTCATCATCAATGGTG  
GTGAACGTATTATCGTTTCTCAGTTGGTCCGCTCACCAGGTGTTTACTTTAACGACAAAG  
TAGACAAAATGGTAAGGTGGGCTATGGTTCAACTGTTATCCCTAACCGTGAGCTTGGT  
TGGAACCTGAAAGCGACTCAAAGATATCACCTACACTCGTATCGACCGTACTCGTAAGA  
TTCCATTTACAACCTTGGTTCGTGCTCTTGGTTTCTCAGGTGATGATGAAATCTTTGATA  
TTTTTGGTGACAGCGAATTGGTTCGCAACACTGTTGAAAAAGATATCCACAAGAATCCAA  
TGGACTCTCGTACAGACGAAGCCTTGAAAGAAATTTACGAACGCCTTCGTCCAGGTGAGC  
CTAAGACGGCTGAAAGCTCACGTAGCTTGCTTGTTGGCTCGCTTCCTTGAACC



## ORF Predictions:

ORF #	Start	End	Direction	Length
6	414	1070	F	219 aa

[SEQ ID NO: ] 3864954-6 ORF translation from 414-1070,  
direction F  
VFEDVLPISNFTDTMELEFVGYEIKEPKYTLLEARIHDASYSAPIFVTFRLINKETGEIK  
TQEVFFGDFPIMTEMGTFIINGGERIIVSQLVRSPGVYFNDKVDKNGKVGYGSTVIPNRG  
AWLELESDSKDITYTRIDRTRKIPFTTLVRALGFSGDDEIFDIFGDSELVRNTVEKDIHK  
NPMDSRTDEALKEIYERLRPGEPKTAESSRSLVGS LP\*

## Blastp and/or MPSearch Result:

## Description:

DNA-DIRECTED RNA POLYMERASE BETA CHAIN (EC 2.7.7.6)  
(TRANSCRIPTASE BETA CHAIN). - BACILLUS SUBTILIS.

Assembly ID: 3864962  
Assembly Length: 902bp

[SEQ ID NO: ] 3864962 Strep Assembly -- Assembly  
id#3864962  
GAATTGAGTGTAAGAAGATATGAGGATCCCTTTAGGGATAGTGGTAAGTAATACCAAAGT  
CTCTTAAAGAGGCAAGTGACGAGTCAAGAGCAATAAGGCTTGAACAACGTGAAAGCCAGC  
GTCTTTAGGCGCTGGCTGATGATTTGGGCTTATAGCTCTGAGATAAACCACCCGTTAGAC  
AGGTGGTTATGATTTTATCTGAGTGTAACATACTGTTGGGCAATCTCGCTGATGCGGTCA  
AAGTTGCCTTGGGAAGCGAGTTTATTGAGTTCGCCACCAATTCCAACGGCGTCTGCACCA  
GCAGCGAACCATTGAGGGATGTTGTTTAGACCGACTCCTCCGGTTACCATTACGGAAACT  
TGTGGGATCGGTGCCTTGACTGCAGAGATATATGCTGGACTGAGAGTACTACTTGGGAAG  
AGTTTGATGATTTCACTACCGGCTTCAAGTGCAGTCGTGATCTCTGTGAGGGTAATACAG  
CCTGGAATGTACGGTGTGCTGTAGAGATTGCACATTTTCGCAGTTTCAGCATGGAAAGAT  
GGAGAAACAACGTAATTTGCTCCGGCTAGAATGGCATCTCTAGCAGTTACGGCATCAAGC  
ACAGTACCTGCACCGATACAAACACTCTTATCGTCCTGATACAAGTCTACAAGTTCCTTG  
ATGATTTGTCCTGCATACTGATTGGTATAGGCGATTTCAATAGCTTTGATACCGCCCTTG

ATACAAGCAATCGAGGCTTGCAGTCCTTCTTCCTTTGTATTTCCCCGAATGACAGCGACA  
 ATTTTCGATGTTTTTTTAGTTCAATAATCGTATCTGATTTGGTCATGTAATTCTCCTAAC  
 GAATGATATCTTGTGCATTTGCCAGTAAATTTTCAATACTAGTTGCGGAAGTGGAGAGAT  
 GG

## ORF Predictions:

ORF #	Start	End	Direction	Length
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6	195	602	R	136 aa

[SEQ ID NO: ] 3864962-6 ORF translation from 195-602,  
 direction R  
 VLDAVTARDAILAGANYVVSPSFHAETAKMCNLYSTPYIPGCITLTEITTALEAGSEIIK  
 LFPSSSTLSPAYISAVKAPIPQVSVMTGGVGLNNIPQWFAAGADAVGIGGELNKLASQGN  
 FDRISEIAQQYVTLR\*

## Blastp and/or MPSearch Result:

## Description:

2-keto-3-deoxy-6-phosphogluconate aldolase (eda) homolog -  
 Haemophilus influenzae (strain Rd KW20)

Assembly ID: 3864970

Assembly Length: 1755bp

[SEQ ID NO: ] 3864970 Strep Assembly -- Assembly  
 id#3864970  
 TTGAGTTAGTACCAATGGACCGACAATTAAAAAGTCATGTTTGCTGATTTTTCAGAAAAT  
 CCTTATCCAGAAATGGAAGAGCAGATGAGGCTGATTGACGAGTGTGGTCCTGAACCTTTAT  
 TTTAAGAACTTAACCTCAAGCAACATTTAGTCCTGAAACGAATAAAAAAATCTGGGAATTA  
 ATGCAAGAAAAAGGCTTAGAGTTGGAAAATCAAGAATCCAGGAATTCAGGATATCTGGG  
 AGAGATTACTGAGGAAGATTTTGAGAATTTGTCGGATAGAATCTCATGTCCCTGTATTTA  
 TTTTTTGTGACAGACTTATAGAGAAAAAGAGTACAGAGAATCAGAATATTGGACTTCCAATA  
 CTAAACTCATTTTAGGAAGGAATCACCATTATTTACAATGGTCAGAATCGGAAAAAATTG  
 CGGCTATTATTCGAGAATTGTCAGAATAAGATGGAAAAAAGGAGATTACAGGAGACAAGA

TGAACTACTTTAATGTTGGGAAAATCGTTAATACGCAGGGATTACAGGGTGAGATGCGAG  
TCTTGTCTGTGACGGATTTTGCAGAAGAACGGTTTAAAAAAGGAGCTGAGCTGGCTTTGT  
TTGATGAAAAAGATCAGTTTGTCCAAACAGTGACCATCGCTAGCCACCGTAAACAGAAGA  
ACTTTGACATTATTAAATTCAAAGATATGTACCATATCAATACTATCGAAAAGTACAAGG  
GATACAGTCTCAAGGTCGCTGAGGAAGATTTGAATGACCTAGACGATGGTGAATTTTACT  
ATCACGAGATTATCGGTTTGGAAAGTCTATGAGGGTGATAGCTTGGTTGGAACCATCAAGG  
AAATCCTGCAACCAGGTGCTAATGATGTCTGGGTGGTCAAACGAAAAGGCAAACGTGATT  
TGCTTTTACCTTATATCCCACCAGTGGTTCTCAATGTTGATATTCCAAATAAACGGGTCTG  
ATGTGGAAATCTTAGAAGGGTTAGACGATGAAGATTGATATTTTAAACCTCTTTCCAGAG  
ATGTTTTCTCCACTGGAGCACTCAATCGTTGGAAAGGCTCGAGAAAAAGGGCTCTTGGAT  
ATCCAGTATCATAATTTTCGAAAAAATGCTGAAAAGGCCCGTCAAGTTAGATGATGAACC  
CTACAGAGGCGGTCAGGGCATGTTGATCAGAGCACACCTATTATCGAATTCCCTTAGATG  
CTATTGAAAAGAAAAATCCGCGCGATATTCTCCTCGATCCTGATGGAAAGCAGTTTGATC  
AGGCTTATGCTGAAGATTTGGCTCAAGAGGAAGAGCTAATCTTTATCTGTGGGCACCTTAT  
GAGGGTTATGATGAGCGCATTAAGACCTTGGTAACAGATGAGATTTCCCTAGGCGACTAT  
GTCCTCACTGGTGGAGAATTGGCAGCTATGACCATGATTGATGCTACAGTTCGCCTGATT  
CCAGAAGTGATTGGCAAGGAGTCTAGCCACCAAGATGATAGTTTTTCTTCAGGTCTTTTA  
GAATATCCTCAGTACACACGTCCCTATGATTATCGAGGCATGGTCGTGCCAGATGTATTG  
ATGAGTGGCCACCATGAAAAGATTCGTCAAGTGGCGATTGTACGAGAGTTTAAAGAAAACC  
TACGAGCGCAGACCAGATTTACTTGAACATTATCAACTGACAGTAGAAGAAGAAAAAATG  
CTGGCAGAAATCAAAGGAAACAAAGAATAAAGGAGAAACCTATGCAAGTAATCAAACGTA  
ATGGCGAAATTTCGAT

## ORF Predictions:

ORF #	Start	End	Direction	Length
7	1309	1710	F	134 aa

[SEQ ID NO: ] 3864970-7 ORF translation from 1309-1710,  
direction F

VGTYEGYDERIKTLVTDEISLGDYVLTGGELAAMTMIDATVRLIPEVIGKESSHQDDSF  
SGLLEYPQYTRPYDYRGMVVPDVLMSGHHEKIRQWRLYESLKKTYERRPDLEHYQLTVE  
EEKMLAEIKGNKE\*

## Blastp and/or MPSearch Result:

## Description:

tRNA (guanine-N1)-methyltransferase (trmD) homolog -  
Haemophilus influenzae (strain Rd KW20)

Assembly ID: 3865012  
 Assembly Length: 1130bp

[SEQ ID NO: ] 3865012 Strep Assembly -- Assembly  
 id#3865012  
 ATCGAATTCCATAAATCTTTTCCTTCCAGATACCCAGACAGGCAATCTCTTCTGGAAGTT  
 CAACGGCCTTATCCGTCTCGCACACAACCATAACATCTTCAGAAAAAGCTCTCTCTCAG  
 CCATTTTTTCAATATCTGCTACGATTTGTTTCCTTGGCATAGGGAGGGTCTAAGAAAACGA  
 GGTCAAATTCCCCAGATAACCTGTTCCAATGCCCTTTCTGCATCCATTTTGGAGGAGTTG  
 AAATTTTCCAACCTTCCTTGGTCATCTGGATATTTTCAGCCACGATGGTCTGAGCCTTACG  
 GTCTCGCTCCACAAAACAGCACTGGACATGCCACGCGATACTGCTTCGATAGATAAACC  
 ACCACTACCTGCATAAAGGTCCAAGACTCGTCCCACTTCAAAGTAGGGACCAATCATGTT  
 AAAAATGGCTCCCCTAACCTTATCCGAAGTAGGTCTTGTTGTCTTGCCTTCTAGTGTCTT  
 GAGGGGACGTCCCCCATAGATTCTTGATACGATTTTCATACTGTTTATTATACCAAATTA  
 TAGACAAAAAGAGAAAGAAAACCGAACCTTGCGGTTTCGATTCTCTACAAAATATTTTCGT  
 AAGTATCGCGGACTTCTTGAGGCCAAACACTTGTTTGCACCTTCTCCGATGTGTCTCTTGC  
 GAAGTAGGAACATGGCCATACGAGATTGTCCAATTCCTCCACCGATTGTCAATGGGAATA  
 GGCCATTCAACAAAGACTTGTGCCATTCCAATTCTAAGCGGTCTTCATCACCTGTAATTT  
 CCACCTGACGTCTAAGAGTTTCTTCATCTACACGAATTTCCCATAGAAGACAACCTCAAAGG  
 CTCCACCTAAAGACTCATTCAGACAAGAATATCACCATTTAGACCCTTGTAGCCATTCT  
 CAGACTCGCTTGTCAGTCATCATAGTCTGGTGCACGTCCATCGTGCGGTTTACCATCTT  
 GGCAACTCGCCACCGATACCAATCAAAAAGACGGCTCCAAATTCTTTACAAATCGCATTT  
 TCCACGTTCTTTAGGTGTCAAGTCTGGGTAGCGTTCTACCAATTCTTCTGTATGGATAAA  
 GGTGATTTGTTTGGCAAGATAGACTCGATGTCATAGCGGGCTTCAACAG

# ORF Predictions:

ORF #	Start	End	Direction	Length
7	584	973	R	130 aa

[SEQ ID NO: ] 3865012-7 ORF translation from 584-973,  
 direction R  
 VASCQDGKPHDGRAPDYDDWTSESENGYKGLNGDILVWNESLGGAFELSSMGIRVDEETL  
 RRQVEITGDEDRLLELHWSLLNGLFPLTIGGGIGQSRMAMFLLRKRHIGEVQTSVWPQE  
 VRDTYENIL\*

Blastp and/or MPSearch Result:

Description:

asparagine synthetase A (asnA) homolog - Haemophilus  
influenzae (strain Rd KW20 )

Assembly ID: 3865148

Assembly Length: 1825bp

[SEQ ID NO: ] 3865148 Strep Assembly -- Assembly  
id#3865148

TATAACCACCAGGCTCATGACTATAGTCTTTTATTTCTTCTGTAAAAGACTGGTCTTGCA  
GATGGCGGTGCAGGCCAACTGGTCCCTTCGATATAACCCATGATTCTTCCTTCTTTTTCAG  
CAACCAGAAAAGAGGTCTGAATTTCTCTCAAATGTGCTTCAAAGACAGAAGGAGGAATGG  
CTTCTTCGACCGAAAAATTATCAAATTCAGTTCAACAATCCGATCCAAATCTTCTAATC  
TTGCTTGTCTGATTTTTCATTGTTCCCTCCAGATAAAAGGGATTAAACCAAATCATACTATA  
GCCCTGGCTAGTTACATAGAGCAAAGTTTCTTCTTCATCAACAAAACCGTTCATTTCAAA  
ATAGGAAAGCAGCTCATCAGGACTCTCCAAACGAATCCCTTTGTAATCCAGCTCAACTGC  
CACCTCTTTCAAGGCTGCAAGAAGAAGTGTTCCAGGCCCTGTCTCTGATGGTCAGACTC  
GATGACTAAAGAATGTACTTTTAGACATTGCGGATTGTCTGACTGGGGACTTGATAAAAT  
ATAGCCTAAAAGTTGATTTTCATCCCTAGCTAGAAGAAAGGTATCCGCACACTTACGGAT  
ACTTTCTTCTAAAATATGGGAAAGTTGCTGCTTTTCAGCTGGAAAAGACGAGGTCTGAAG  
TGCCCCCTATCTCAGGCAAATCAAACCTTGCTTGCCCTGAATGATCTTAATTGGAATTTCCAT  
GGGAAACATCCTATTGAACATTGCTTGCTCAAGTTAGACAAGAGACGCTCAAATGAGTATT  
CATAGGTTTGGATGTCTCCTGCTCCCATAAAGACGTAAACAGCATTGTCATGGTCTAGGA  
GTGGAGAAACATTTTCAACAGTAATCACTTGGTGTTTTTTGTTGATTTTATTGGCTAGGT  
CTTCTACCTTAACGTCACCATGATCTACTTCACGAGCCGAGCCATAAATTTGCGCTAGAT  
AAACAGCATCTGCTTGGTTTAAAGCATGGGCAAAGTCGTCCAACAGGGCAATGGTTCTTG  
TAAAGGTATGCGGTGGAAAGAACTGCTACAATTTCTTGGCTTGGGTATTTCTGACGAGCC  
GCATCCAAGGTCGCAATAATTTCTGTTGGATGATGGGCAAAGTCATCAATAATCACTGTA  
TCATTGACAATTTTCTCAGTGAAACGACGTTTAAACACCGGCAAATGTTTTCAAGTGCTCA  
CGCACCAAGTTCAAATCAAATCCTGCTGTGTAAAGAAGACCAATAACGGCTGTGCGATTC  
ATGATATTGTGACGACCAAAGGTTGGAATGTGGAATTGCCCCAAGTTTTGTCCACGGAAA  
TGAACGGTGAAGGTTGAACCAGTTGTTGAACGAAGAAGATCACTAGCTACAAAGTCATTG  
CCTTCAGCTTCAAACCATATAATAAATTGGTGCATCAGACGTAATCTTACGCAATTCA  
GCATCTTCACCATAGACAAAAAGACCCATCGTAATTTGTTTGGCATAGTCGTTAAAGGCA  
TTGAAAACATCCTCGAGACTTGTGAAATAATCTGGATGGTCAAAGTCAATGTTGGTGATA

ATAGAGTATTCTGGGTGGTAAGGCATGAAGTGACGCTCATATTCGTCAGATTCAAAGACA  
AAATATTTGGCATTGGCCGAACCACGACCTGTCCCATCTCCAATCAAGAAGCTGGTATCT  
GTAATGTGAGACAAGACATGAGACAACATACCTGTCGTTGAAGTTTTTCCATGTGCTCCT  
GCTACTCCCATGCTAACAAAGTCACGCATAAAGCTACCTAGAACTCATGGTAACGTTTG  
TAGCTGATACCATTTTGGTCCGCAT

## ORF Predictions:

ORF #	Start	End	Direction	Length
6	256	423	R	56 aa
7	731	868	R	46 aa

[SEQ ID NO: ] 3865148-6 ORF translation from 256-423,  
direction R  
VAVELDYKGIRLESPDELLSYFEMNGFVDEEETLLYVTSQGYSMIWFNPFYLEEQ\*

## Blastp and/or MPSearch Result:

Description:  
unknown

[SEQ ID NO: ] 3865148-7 ORF translation from 731-868,  
direction R  
VITVENVSPLLDHDAVYVFMGAGDIQTYEYSFERLLSNLTSNVQ\*

## Blastp and/or MPSearch Result:

Description:  
UDP-N-ACETYLMURAMATE--ALANINE LIGASE (EC 6.3.2.8) (UDP-N-  
ACETYLMURANOYL-L-ALANINE SYNTHETASE) (FRAGMENT). -  
BACILLUS SUBTILIS.

Assembly ID: 3865178  
Assembly Length: 1002bp

[SEQ ID NO: ] 3865178 Strep Assembly -- Assembly  
id#3865178

ATCGAATTAAGGTAAAACTAAAAGGACTTAGTCCTGTGCAGTACAGAACTAAATCCTTCG  
GATAGAATTATTTGTCTAACTTTTTGGGGTCAGTACACCTAAAACTTTGATGATATACGT  
TTCCTTGTGAGAATATTTACTTCATTTTTGCCTAAAATTCAATGTTTACTCAGTATTTGG  
ATTATGAAAAATCGAGGTCTAAATCTAGATACATTTTTTCTGAAGACAAATCATTTTGAC  
CACCGAGCAAGAGATTTTCAAAAAAAGCTGTTAAAAACTCAGAACGTCGCTGTAAAATCT  
TTGCATTATCTAATACCAAGGCATCACGAAAATATTTGGAATGTTGCTGAAATGGTGTAT  
TATCAATATCAAAACCAAACCTCACGAAGATACTGAATCAAAAAGACCGTTACTGTCCGAG  
TGTTTCCTTCGCGAAATGGATGAATCTGCCAGATTCCTGAAATAAAATGCTGGATTTGTT  
TAACCACATCCGCCTGAGTTAGTGTGCGCATATGCAACTTGTTTTCTCTGATTAAAATCAT  
AATCTAAGGTCATTTGAATCATGGAGTAATCAGAGTACACAACACTTTCACCATTCAAAA  
CAGGTTTCATTCCTTTGTGATATTGGTCTGACGAAATTCGATCCACCGGAAATAGAGGGTTC  
AAATATATCTTGAAACAACTCCTTATGAATAGCAAGTAAGGTCGCAGGACTAAAGCTAAA  
GCCTCTTCGAGACAATAGTTCTACAATACGTTAGAGAAACCAAGTCTGCCTCCTTCCCGT  
ACTTGCATCAATAATATGGTGAATAAGCCGGTGCATTCCTCATAAACCTGCTCATAAGTC  
AGTTCTCCCCGGGACTGTTTCTCAGCCAAAGATTCCATATACGCTGATGGCACTAGATTG  
TCAACTTTCTGCAGACCAAAACCTATCCGCCATAAATCACGCTTCGCTTCATAAGACAAG  
TTTGGATTGTCAATGTTGTAAGTTGGTTGCATAAAAAATATCC

#### ORF Predictions:

ORF #	Start	End	Direction	Length
6	182	580	R	133 aa

[SEQ ID NO: ] 3865178-6 ORF translation from 182-580,  
direction R  
VYSDYSMIQMTLDYDFNQEKGQVAYATLTQADVVKQIQHFISGIWQIHPFREGNTRTVTVF  
LIQYLREFGFDIDNTPFQQHISKYFRDALVLDNAKILQRRSEFLTAFENLLLGGQNDLSS  
EKMYLDLDFLDFS\*

#### Blastp and/or MPSearch Result:

Description:  
unknown

Assembly ID: 3865260

Assembly Length: 1250bp

[SEQ ID NO: ] 3865260 Strep Assembly -- Assembly  
id#3865260

CTGTCACTACTCCATTTACTACCGATTGCCATGAACACCAAACCACCACAAAAATGATAT  
AAAGAATGCAATTCCAATAGCACCATACAAAGATCCAGTTAAACCTTGCAACGGAACCTTG  
AATAGCAGAATAAATCATTTCTATGAATGTTCCGCCATTAGTCAATGACTTCGCTAAAAT  
ATATACAATCATAGAAGATAAGAAAATTACAAATGCTGGAATCATTGCTTCAAACCTGTTT  
GGCAATAGCTTGTGGAACCTGTTCTGGCATCTTAATAACAATTTTTCTCTTTATAAAGAA  
GGTATAAATACTTCCTACTACCAAACCTATAATGATAGCACCGATAATTCCTTGGCCTC  
CAAACCAAACCTTTACTAATAGCGTCCCCAATCGCCTCACCTTGTTTAGGGATATAAGATG  
ATCTTAGCAAAATAAAGAATGCAGATACAGATAGAACTCCAGCTGGTAAAGCCTCTACTC  
CGCTATTCTTAGCATAAGAATAGGCAATTGAAAAACAAGAAATTAGACCCATAATAGCAA  
AAGTTCCTGAATATACTTGCATAAACGGCTCTGTCCAATTAGCTCCAAAAACACTAGCAA  
TGCTCTTATTTAATCCTTCGAACGGCAATTGTCCCATAATCAAGAACAACTACCAACTA  
CTGTCAATGGCAAAATTGCTAACATCCCATCTTTTAGAGCTATAATGCCACGCATATTCA  
CAAACCTTCATCATCGGTGCAATGATTTTCTGAACATCCATCTTTGACATAATAAATCTCC  
TTTTCTTACCCACTAATCAAAGATAGGGCCAAATCTAATACTTTTTTCCCATCTAACATA  
CCATAGTCCATCATCGGAATAACAGCTATCGGAACATCACACTTATCACAAATTTCTTTT  
GATTTATCTAATGTATAAGCAACTTGTGGACCCAATAGTGCAACATCTATATTTGGCGCA  
TAATCCGCTAATTTAGACTGAGAAAACGCCTCTATTTCTGCCTCAACTCCACTAGCTTGC  
GCTGCAATTTTCATATTATTTACAAGCATACCAGTAGAAAAAACCTGCTGCACAAAACAA  
ACCAATCTTCACCATTTATGTTTTCTCCTCTATGTTAATAACAATGATAATACTCTAGTA  
ATAATTTTTTATGAAGTTTCTTTTCTCAAATAAATAATTTCTTTGAATTAAATTAATC  
TCCGGTCATACTAGTCCATGAAAANGATCTTGTGAATGAACCAAGAAGAG

#### ORF Predictions:

ORF #	Start	End	Direction	Length
6	19	399	R	127 aa
7	272	793	R	174 aa
8	786	1073	R	96 aa

[SEQ ID NO: ] 3865260-6 ORF translation from 19-399,  
direction R

VRRLGTL LVKFGLEAKGIIGAIIGLVVGSIIYTFIKRKIVIKMPEQVPQAIKQFEAMI



PAFVIFLSSMIVYILAKSLTNGGTFIEMIYSAIQVPLQGLTGSLYGAIGIAFFISFLWWF  
GVHGNR\*

Blastp and/or MPSearch Result:

Description:

cellobiose phosphotransferase system celB - Bacillus  
stearothermophilus

[SEQ ID NO:     ]     3865260-7 ORF translation from 272-793,  
direction R  
VGKKRRFIMSKMDVQKIIAPMMKFVNMRGIIALKDGMLAILPLTVVGSFLIMGQLPFEG  
LNKSIASVFGANWTEPFMQVYSGTFAIMGLISCFSIAYS YAKNSGVEALPAGVLSVSAFF  
ILLRSSYIPKQGEAIGDAISKVWFGGQGNRYCYHYRFGSRKYLYLLYKEKNKY\*

Blastp and/or MPSearch Result:

Description:

cellobiose phosphotransferase system celB - Bacillus  
stearothermophilus

[SEQ ID NO:     ]     3865260-8 ORF translation from 786-1073,  
direction R  
VQQVFSTGMLVNNMKIAAQASGVEAEIEAFSQSKLADYAPNIDVALLGPQVAYTLDKSKE  
ICDKCDVPIAVIPMDYGMLDGKKVLDLALSLISG\*

Blastp and/or MPSearch Result:

Description:

cellobiose phosphotransferase system celA - Bacillus  
stearothermophilus

Assembly ID: 3865272  
Assembly Length: 1164bp

[SEQ ID NO: ] 3865272 Strep Assembly -- Assembly  
id#3865272

AATGTAATGCGGCGAGCAAGGACGTGAAGACGCCTTTGTAGATCCACTTGCAGATATTGA  
TACAATTAATCTGGAATTAATTCCTTGCTGACTTAGAATCAGTGAACAAACGATATGCGCG  
TG TAGAAAAGATGGCACGTACGCAAAAAGATAAAGAATCAGTAGCAGAATTCAATGTTTC  
TTCAAAAGATTAAACCAGTCCTAGAAGACGGGAAATCAGCTCGTACCATTGAATTTACAG  
ATGAGGAACAAAAGGTTGTCAAAGGTCTTTTCCTTTTGACGACTAAACCAGTTCTTTATG  
TAGCTAATGTGGACGAGGATGTGGTTTCAGAACCTGACTCTATCGACTATGTCAAACAAA  
TTCGTGAATTTGCAGCGACAGAAAATGCTGAAGTAGTCGTTATTTCTGCGCGTGCTGAGG  
AAGAAATTTCTGAATTGGATGATGAAGATAAAAAAGAGTTTCTTGAAGCCATTGGTTTGA  
CAGAATCAGGTGTAGATAAGTTGACGCGTGCAGCTTACCACTTGCTTGGATTGGGAACCTT  
ACTTCACAGCTGGTGAAAAAGAAGTTCGCGCTTGGACTTTCAAACGTGGTATGAAGGCTC  
CTCAAGCAGCTGGTATTATCCACTCAGACTTTGAAAAAGGCTTTATTCGTGCAGTAACCA  
TGTCATATGAAGATCTAGTGAAATACGGATCTGAAAAGGCCGTAAAAGAAGCTGGACGCT  
TGCGTGAAGAAGGAAAAGAATATATCGTTCAAGATGGCGATATCATGGAATTCCGCTTTA  
ATGTCTAAAAATTAATAAATGGTGTCAATTAGGTTGGAAAAAAATTCCAACCCTTTTGGC  
TTTTGAAAGGAAAAATAAATGACCAAATTACTTGTAGGCTTGGGAAATCCAGGGGATAAA  
TATTTTGAAACAAAACACAATGTTGGTTTTATGTTGATTGATCAACTAGCGAAGAAACAG  
AATGTCACTTTTACACACGATAAGATATTTCAAGAATTCGGACCTAGCATCCTTTTTCTT  
AAATGGAGAAAAAATTTATCTGGTTAAACCAACGACCTTTATGAATGAAAGTGGAAGC  
AGTTCATGCTTTATTAACCTACTATGGTTTGGATATTGACGATTTACTTATCATTTACGA  
TGATCTTGACATGGAAGTTGGGAA

#### ORF Predictions:

ORF #	Start	End	Direction	Length
6	101	193	F	31 aa

[SEQ ID NO: ] 3865272-6 ORF translation from 101-193,  
direction F  
VNKRYARVEKMARTQKDKEVSAEFNVSSKD\*

#### Blastp and/or MPSearch Result:

Description:  
unknown

Assembly ID: 3865280  
 Assembly Length: 1320bp

[SEQ ID NO: ] 3865280 Strep Assembly -- Assembly  
 id#3865280

CGAATTCAGGTTTCTTTGTTTGTCTTCATTCGTTTACGTTTAATCTTTGAATCGAGG  
 GATGATGTTCTTTTGAAGCAATTAGTTTTAGAATCATCTACTGAGGTTATTAAATCTGTA  
 GAGGTAGAGAGTTTTGAGTTTGAAACAGGAAGACAATATTTTCTATCCGGAAGAAGACAA  
 GATTGTATTAAGGAAATGGCGAATTTTTCCGGTTATTATCTACGAATTGGGACCACCTGT  
 TTATCCCAATTCTTTATTCTTAGGAATGGAATTTCCAATGTCTGAAAACAAGGTAGATGG  
 TAGACACTATGTATCAAGATATTACTTGGGAAGTGTGTAAATCACCAGGAGGTTTG  
 TGGTCTTGTTATTATTGGGGGAGCATGTTCTTATAAAAAAGAAGAGATTCAAGAGGCATTT  
 TTTGAATATGTTGAAGGAATAGCTCAACCTAGTTATTTCCGTAAACAGTATAATTCCTGG  
 TATGACCATATGACCGATATTACAGAGGAAGGTATTTTAAAAAGTTTTTCTGAGATTCGA  
 GATGGATTTGAAAATCATGGAGTTCATTTAGATGCTTATGTTGTTGATGATGGTTGGACA  
 AACTATCAATCAGTTTGGGAATTCATCATAAATTCCTCAATGGTTTGAGAAATATTAAA  
 TATCTTGTAATGGATTTGGTTCCAACCCTAGGATTGTGGATTGGTCCCCGAGGTGGTTA  
 TAATGGGACAGAAATCATTATGAGTTGATTGGTTAGAAGCACATCCCAGAGTTTAAATAT  
 TGGATCTAAAAATTTGATTTCAAATGATGTAAACGTGGCTGATTTTAACTATCTCAATCA  
 AATGAAGAAAAAGATGTTGGAATATCAAAAAGAATTTCGATATCAGCTATTGGAAAATTGA  
 TGGTTGGTTACTTCAACCTGACAAACCTGATAAGAGTGGACCGCACGGTATGTATACCAT  
 GACAGCGGTTTATGAGTTCTTAATTCAACTGTTGATAGATCTAAGAAAGGAGAGAGGAGG  
 AAAAGATTGTTGGTTAACTTGACTTCTTATGTAAATCCTAGTCCATGGTTTTTACAGTG  
 GGTCAATAGTTTATGGATTCAAATATCTCAAGATGTAGGCTTTACAGAGAATGCAGGTAA  
 TGATATCAATCGTATGATTACTTACCGAGATAGTCAGTATCAAGAATTTTTTGGGAAAAAC  
 GTGAGATACAGTTACCTATGTTGGGTCGCTTTTATAAATCATGAACCAATCCTATGCTGT  
 CAGTGCCAAATACCTGGTACATGGATCATCAAATGTTTGCATCAATACCAGATTTTGAAG

#### ORF Predictions:

ORF #	Start	End	Direction	Length
7	815	1204	F	130 aa

[SEQ ID NO: ] 3865280-7 ORF translation from 815-1204,  
 direction F  
 VADFNLYLNQMKKKMLEYQKEFDISYWKIDGWLLQPDKPKDSGPHGMYTMTAVYEFLIQLL  
 IDLRKERGGKDCWLNLTSYVNPSPWFLQVWNSLWIQISQDVGFTENAGNDINRMITYRDS

QYQEF LGKT\*

Blastp and/or MPSearch Result:

Description:  
unknown

Assembly ID: 3865286  
Assembly Length: 1305bp

[SEQ ID NO: ] 3865286 Strep Assembly -- Assembly  
id#3865286

CTTAGAAGAAAAGGCTGAGGGCAAATACTAGTCTGTGCGAGTTTCTTCTGTCATTGCGCG  
TGATCTCTTTCTGGAAAATCTTGAAAATCTGGGACGAGAACTGGGTTATCAGCTTCCAAG  
TGGAGCTGGAACGGCTTCTGACAAGGTGGCTAGCCAGATTTTGCAAGCCTATGGTATGCA  
GGGACTCAACTTCTGCGCCAAATTGCACTTTAAAAACACTGAAAAAGCGAAAAACGCTT  
AGAAAGGTAAGTTATGAATTCATTTAAAAATTTCTTAAAAGAGTGGGGACTGTTCCCTCCT  
AATTCTGTCATTACTAGCTTTAAGTCGTATCTTTTTTTGGAGCAATGTTTCGCGTAGAAGG  
ACATTCCATGGATCCGACCCCTAGCGGATGGCGAAATTCTCTTCGTTGTAAAACACCTTCC  
TATTGACCGTTTTGATATCGTGGTGGCCCATGAGGAAGATGGCAATAAGGACATCGTCAA  
GCGCGTGATTGGAATGCCTGGCGACACCATTTCGTTACGAAAATGATAAACTCTACATCAA  
TGACAAAGAAACGGACGAGCCTTATCTAGCAGACTATATCAAACGCTTCAAGGATGACAA  
ACTCCAAAGCACTTACTCAGGCAAGGGCTTTGAAGGAAATAAAGGAACCTTCTTTAGAAG  
TATCGCTCAAAAAGCCCAAGCCTTCACAGTTGATGTCAACTACAACACCAACTTTAGCTT  
TACTGTTCCCAAGGAGAATACCTTCTCCTCGGAGATGACCGCTTGGTTTCGAGCGACA  
GCCGCCACGTTAGGTACCTTCAAAGCAAAAGATATCACAGGGGAAGCTAAATTCCGCTTC  
TGGCCAATCACCCGTATCGGAACATTTTAAGAAACCTAAGAGGCCGAGAATCACCAATCT  
CAGCCTCTTCTTCTATCGTGAGAAAATGATTGGTACTATCTAAACTTACCAGAACAGAAA  
CACCTCAACTCTCACCTATTCATGCAAAGGAATTCGATGGAAGTTTATTTTTCAGGAACT  
ATTGAACGGATTATTTTTGAAAATCCCAGCAATTTTTATCGCATCCTCCTCCTAGAAATC  
GACGATACGGACGCAGAGGATTTTGATGATTTTGAAATCATTGTCACAGGAACCATGGCT  
GATGTAATTGAGGGCGAAGACTATACTTTTTGGGGGCAAATTTGTCCAGCACTCCAAGTAT  
GGAGAACAACCTGCAAATCAGTCGTTATGATCGCGCAAAACCAACTAGTAAGGGCTTGGTC  
AAGTACTTTTCAAGTAGCCATTTCAAGGGATTGGTCTCAAGACAG

ORF Predictions:

ORF #	Start	End	Direction	Length
6	146	250	F	35 aa

[SEQ ID NO: ] 3865286-6 ORF translation from 146-250,  
direction F  
VASQILQAYGMQGLNFCAKLHFKNTEKAKKRLER\*

Blastp and/or MPSearch Result:

Description:  
unknown

Assembly ID: 3865326  
Assembly Length: 804bp

[SEQ ID NO: ] 3865326 Strep Assembly -- Assembly  
id#3865326  
CTATGCTTGTAAGGGCTTTGCTTTCAGGATCAGTTGCCTTACTTGTCGGCATTC AACCT  
TGGTCTTGAAGGGGACTATCTTGCGGTAGCAACTCTGGGTGTTTATCGAAATTATCCGT  
ATCTTTATCATCAATGGTGGAAAGTCTTACAAATGGTGCGGCAGGTATCTTAAGGATTCCT  
AACTTTACAACCTGGCAAATGGTTTACTTCTTTGTCTGATTACAACCATTTGCAACCTTG  
AACTTCTTGCGTAGCCCAATTGGACGTTCAACCCTCTCTGTTTCGTGAAGATGAAATCGCT  
GCTGAGTCAGTTGGGGTTAATACGACTAAAATTAAAATCATCGCTTTTGTCTTTGGTGCC  
ATTACTGCAAGTATTGCTGGGTCACTTCAGCCAGGATTAATCGGGTCTGTTGTACCGAAA  
GATTACACCTTCATCAACTCAATCAACGTTTTGATTATTGTTGTATTTGGTGGACTCGGT  
TCCATTACAGGTGCGATTGTTTCGGCTATTGTTTCATCGAATTTTGAATATGCTTCTCCAA  
GATGTTGCTAGTGTGCGTATGATTATTTACGCTTTGGCCTTGGTATTGGTAATGATTTTC  
AGACCAGGTGGACTCCTTGGAACGTGGGAAGTGAAGCTATCACGTTTCTTTAAAAAATCT  
AAGAAGGAGGAACAAAATAATGGCATTACTTGAAGTAAAACAGTTAACCAACATTTTG  
GTGGTCTAACAGCTGTTGGAGATGTGACTCTGGAATTGAACGAAGGGGAACTGGTTGGAT  
TAATCGGTCCAAACGGAGCTGGGA

ORF Predictions:

ORF #	Start	End	Direction	Length
				159

-----  
 7            100            681            F            194 aa

[SEQ ID NO:     ]     3865326-7 ORF translation from 100-681,  
 direction F

VFIEIIRIFIINGGSLTNGAAGILRIPNFTTWQMVYFFVVITTIATLNFLRSPIGRSTLS  
 VREDEIAAESVGVNTTKIKIIAFVFGAITASIAGSLQPGLIGSVVPKDYTFINSINVLII  
 VVFGGLGSITGAIVSAIVHRILNMLLQDVASVRMIIYALALVLVMIFRPGLLGTWELSL  
 SRFFKKSKEEQN\*

Blastp and/or MPSearch Result:

Description:

HIGH-AFFINITY BRANCHED-CHAIN AMINO ACID TRANSPORT PROTEIN  
 BRAE. - PSEUDOMONAS A ERUGINOSA.

Assembly ID: 3865438  
 Assembly Length: 553bp

[SEQ ID NO:     ]     3865438 Strep Assembly -- Assembly  
 id#3865438

CCCATCTGCCTTGACCAAAGGCTACCACTTCAAACTCGCCTCACCTTGGAATTTTCA  
 GCTTTAGATGGGCATTACCTGCCCCAGTAGTACGAGCACTTTCGACCTGAAAATTCTTG  
 ATATAAAAAATAGGTTTCTGATTATCCATTCCAAAAGGAGCTAAACGTTCAAACTTTTG  
 ACCGTTTCCAAGCTAAGTGCCTCCAAATCCAACCTCTTCATCTAGGTTTAACTTATTCTTT  
 CCACCAGCATCTGCACCTTTTTCACGAACATAATCTTCCAAAACCTGAGATAAATCTGAG  
 AGTTGCTCAACTTCCAGCGTCATACCCGCTGCACCTGCATGACCTCCAAAGGCGATGAAG  
 AGGTCTCGATGGGGATCCAGAGCTTCAAAAATATCGACCGCTTCCACACTACGAGCACTG  
 CCCTTGGCACGACCGTCTTCTATATTAAGAAACAATGACTGTCTGTCCCAATTCTTCCAA  
 TAAACGACCAGCCACGATTCCTAGAACCCAGGATTCAGCCTTCCTTGGCCAAGACCTG  
 AACTTTTCTCAG

ORF Predictions:

ORF #	Start	End	Direction	Length
-----	-----	-----	-----	-----

6 75 407 R 111 aa

[SEQ ID NO: ] 3865438-6 ORF translation from 75-407,  
direction R  
VEAVDIFEALDPHRDLFIAFGGHAGAAGMTLEVEQLSDLSQVLEDYVREKGADAGGKNKL  
NLDEELDLEALSLETVKSFERLAPFGMDNQKPIFYIKNFQVESARTTGGR\*

Blastp and/or MPSearch Result:

Description:  
unknown

Assembly ID: 3865446  
Assembly Length: 965bp

[SEQ ID NO: ] 3865446 Strep Assembly -- Assembly  
id#3865446  
ACATCTTAAGATTAATTTTCAGAATCTTCTCTTGAAGACTTTTTTAAAGTTGGTCGTCTATA  
GGGAGTTTTTGGCCATCGTTGCTCAATTGTCTGATTAAGGTCCTACCCTTGATGAAACAA  
TTATTATCCATGTTTTCTTTATTATAGACAAAGTAAGAAGACGTTTCTCGAATGTAGACT  
TTATATTTTTTATGATTTTCTTCTTCCATAATATCCAATTGATAGTTGGGAATGAAAATA  
AGACCGCTCTGTTTGACACCGAAAGACACCTTGATATAGACGCCCTTATCAACTAGCTTC  
TCTATTTGGTTCTCTGCAAGTTCCACTTCAAATTCACGAACGGTATCTCATTTTTTCCTTA  
AATGTCTTAAAGGCTTCCTCAATCTCTTCAGTGGATACTTTATCCTTATCTCGTTCTTCT  
TGAAAGCATGGTACTGTTCCCTGTAAATTCTCTAATCCTTCTGAAGCAACGACTTCCTTA  
TTTTTAAATAATCTTGAAAAAATTTGACATCATATAATTTCTTATCACTTATTTTTTTGA  
TGACCCAAACTTATCTTTTGATTATTTTCTTCCAGGATAAAAGTTACATTTTTTTGTTTT  
AAGTCAATGGTTAGATTCAATTCTTTTGCTTTTGTTATTAAATCTTCTAAAGAATTGACA  
CGGTTTAAACAAAATTCTAAACGACTTTCAATCTCTTGCTTAGCAAAATGCGTTCTAAAA  
AATTCTTCATCATATAGATCTCGTTTGCTGAGTTGGCGCCCTCGAATTGGTTTTATCATC  
GTTCTATCTGTCTATCAAAAAACGGCTATGCTTTTGACTAAAATCAATCTGAACATGCAAC  
TGCTTTGCTTTCTCTAAAAAATCATCAAACGATTTAGATTGCTGAAGCAAAAAATAAAGA  
CGTTGTTTCAATTCAAATTTATGACTAGATTCCTTATATTTTTTTATAATCTCGATAGGAA  
TAACG

ORF Predictions:

ORF #	Start	End	Direction	Length
6	42	326	R	95 aa

[SEQ ID NO: ] 3865446-6 ORF translation from 42-326,  
direction R  
VELAENQIEKLVDKGVYIKVSFGVKQSGLIFIPNYQLDIMEEENHKKYKVYIRETSSYFV  
YNKENMDNNCFIKGRTLIRQLSNDGQKLPIDDQL\*

Blastp and/or MPSearch Result:

Description:  
unknown

Assembly ID: 3865474  
Assembly Length: 795bp

[SEQ ID NO: ] 3865474 Strep Assembly -- Assembly  
id#3865474  
TCCCAAGCAAATCCTTGATAGCATGGACTTTGCTGTCAACGTTTCATGCCTCCTTCCTTCC  
TAGACACCGTGGTGGTGGCGCTATCCATTATGCCTTGATTCAAGGGGATGAGGAAGCTGG  
TGTGACCATCATGGAAATGGTTAAGAAAATGGATGCAGGAGATATGATTTCTCGTCGCAG  
CATTCGGATCACAGATGAGGACAATGTTGGCACCTTGTTTGAAAAATTGGCGCTAGTTGG  
TCGTGATTTGCTTTTGGACACTCTGCCTGCCTATATTGCTGGTGATATCAAACCTGAACC  
GCAGGATACGGAGTCAGGTTACCTTCTCTCCAAATATAAAGCCAGAGGAAGAAAACTGG  
ACTGGAACAAAACCAATCGTCAACTCTTTAACCAAATTTCGTGGAATGAACCCCTGGCCTG  
TTGCCCATACTTTTCCTTAAGGGCGACCGCTTTAAGATTTATGAAGCCCTACCAGTAGAAG  
GTCAGGGAAATCCAGGTGAAATTCTCTCTATCGGCAAGAAAGAATTGATTGTCGCAACGG  
CTGAAGGGGCTCTATCCCTCAAACAAGTGCAGCCAGCTGGTAAGCCTAAGATGGACATTG  
CTTCCTTCCTCAACGGAGTTGGACGTACATTGACTGTAGGAGAACGATTTGGTGACTAAA  
GTAGAAACGGCTAGAAGTTTAGCTCTAGCAGTGCTAGAGGATGTTTTTGTGAACCAAGCA  
TATTCAAAATATCGCCTTAAATAAACACCTCAAGGGGAGTCAGCTTTCTGCAGCAGACAAG  
GGCTTAGTGACCGAG

ORF Predictions:



ORF #	Start	End	Direction	Length
6	243	659	F	139 aa

[SEQ ID NO: ] 3865474-6 ORF translation from 243-659,  
direction F  
VICFWTLCLPILLVISNLNRRIRSQVTFSPNIKPEEEKLDWNKTNRQLFNQIRGMNPWPV  
AHTFLKGDRFKIYEALPVEGQGNPGEILSIGKKELIVATAEGALSLKQVQPAGKPKMDIA  
SFLNGVGRTLTVGERFGD\*

Blastp and/or MPSearch Result:

Description:

methionyl-tRNA formyltransferase (fmt) homolog - Haemophilus  
influenzae (strain Rd KW20)

Assembly ID: 3865476

Assembly Length: 816bp

[SEQ ID NO: ] 3865476 Strep Assembly -- Assembly  
id#3865476  
CTGGTAAAATTGAGGAAACCTTGTATGGTCTAAAAGACAAGTACACCATGCTTCTGGTAA  
CCCGTNCCATGCAGCAAGCTTCACGTATCTCTGATAAGACAGGATTTTTCCTAGATGGAG  
ATTTGATTGAATTTAATGATACCAAGCAGATGTTCTTAATCCCCAACACAAGGAAACG  
GAAGACTATATTACAGGAAAATTTGGATAAGGAGATGAAAGATGTTACGATCTCAATTTG  
AAGAAGATTTAGAGAAATTACATAACCAGTTCTACGCTATGGGACAAGAAGTGCTCTCAC  
AAATCAATCCGTACGGTACGTGCTTTTGTACGCATGACCGTGACCTGGCAAAAGAGGTC  
ATCGAAGATGATGCAGAAGTAAATGAATACGAAGTGAAACTGGAAAAGAAATCATTTGAA  
ATGATCGCACTCCAACAACCAGTCTCTCAAGATTTGCGTACAGTCTTGACTGTCCTTAAG  
GCTGTATCAGATGTGGAGCGTATGGGGGATCACGCTGTAGCCATTGCTCAGGCAACCATC  
CGTATGAAGGGGGAAGAGCGCATTTCCAGCTGTAGAGGAAGAAATTAAAAGAAATGGGACG  
TGAAGTTAAAAGCGTTGTTGAAGCAGCACTTGATCTTTATCTTAATGGTTCTGTTGACGA  
CGCATACCGGGTGGCCTCCATGGGATGAGCAAATTAACCACTATTTTGAAACTATCCGTG  
AACCTTGCGACTGAATGAAGATTAAGAAGAGTTCCAATCCAGAAGCCATTGTGACGGGTC  
GTGATTATTTCCAAGTTATTTTCCTACTTGGGAGCGT

## ORF Predictions:

ORF #	Start	End	Direction	Length
6	394	603	F	70 aa

[SEQ ID NO: ] 3865476-6 ORF translation from 394-603,  
 direction F  
 VKLEKKS FEMIALQQPV SQDLRTVLTVLKAVSDVERMGDHA VAI AQATIRMKGEERIPAV  
 EEEIKRNGT\*

## Blastp and/or MPSearch Result:

## Description:

Probable phosphate regulator PhoU homolog

Assembly ID: 3865502

Assembly Length: 1041bp

[SEQ ID NO: ] 3865502 Strep Assembly -- Assembly  
 id#3865502  
 CTGAAATTGCACCACCAGATGGGATTGGGCAGGTTCTCAGCAACCTCTTGCTCAAACCTGG  
 TTGACAACCCAGTCAACGCCCTGCTTACTGCTAACTATATTAGAATCTTATCTTGGGCAG  
 TCATTTTGGGAATCGCTATGAGAGAAGCCAGTAAAAATAGTAAAGAATTGCTAAAACTA  
 TCGCTGACGTGACTTCTAAAATTGTGCAATGGATCATCAATCTGGCTCCATTTGGAATCC  
 TTGGTCTTGTTTTTAAAACCATTTCTGACAAGGGAGTCGGAAGCCTTGCCAACTACGGTA  
 TTTTATTGGTTCTATTAGTAACGACTATGCTTTTTGTTGCCCTGTGGTCAACCCTTTGA  
 TTGCCTTCTTCTTTATGAGACGCAATCCTTACCCTCTAGTTTGGAAGCTGCCTCCGTGTTC  
 AGCGGGTGTGACAGCCTTTTCACTCGTAGTTCTACGACTAACATTCTGTCAACATGAA  
 ACTCTGCCATGACCTTGGACTCAACCCAGATACCTATTCTGTTTCTATCCCACTCGGTTC  
 TACTATCAATATGGCTGGAGTAGCGATTACCATTAACCTTTTGACCCTTGTTACAGTTAA  
 CACTCTTGGAATTCCTGTTGACTTTGCCACAGCCTTTGTCCCTCAGTGTGGTAGCAGCTAT  
 CTCAGCCTGTGGTGCTTCAGGTATTGCCGGAGGTTCCCTCCTTCTTATCCCAGTTGCTTG  
 TAGCCTTTTCGGTATTTCTAACGATATTGCCATACAAATTGTTGGGGTTGGTTTTGTGAT  
 TGGTGTCAATCAAGACTCATGTGAAACAGCCCTTAACCTTCTACAGATGTCTCTTTAC  
 CGCCGTTGCCGAATACGCAGCAACCCGTAAAAATAACTCATCAAGGCAAGCCTGCTTAT

GTCTTGTCTTTTACGCTTTTATTCTAACTTATTAGGAAATTCTTATGTCTATTAGCCAAAC  
 GTACGAACAAGCTCATCTTAGCTACCTGTCTTGCCTGCCTGCTTGCTTATTTTCTCAATC  
 TTTCATCAGCAGTTTCGGCTG

## ORF Predictions:

ORF #	Start	End	Direction	Length
6	428	877	F	150 aa

[SEQ ID NO: ] 3865502-6 ORF translation from 428-877,  
 direction F  
 VTAFFTRSSTNIPVNMKLCHDLGLNPDYSVSIPLGSTINMAGVAITINLLTLVTVNTL  
 GIPVDFATAFVLSVVAASACGASGIAGGSLLLIPVACSLFGISNDIAIQIVGVGVFVIGV  
 IQDSCETALNSSTDVLF TAVA EYAATRKK\*

## Blastp and/or MPSearch Result:

## Description:

Probable sodium-dicarboxylate symporter

Assembly ID: 3865694  
 Assembly Length: 544bp

[SEQ ID NO: ] 3865694 Strep Assembly -- Assembly  
 id#3865694  
 CTGATGACACAAAGCACAGTGGGTAGGACTTGCGAAGTCACCCTTTTCTTTTCAAAATTT  
 ATACTAAATCATTTGATATCAGTGTAGTCACGATTAAGTCCTTGAGCAACTGGTAGGCTAG  
 TCAAGTAACCTTGATAAGTGGTCACACCTTGACGCAAGCCTTCATCTTCAGAGATTGCTT  
 GTGCGAATCCTTTGCCAGCCAAAGCTTCGATATAAGGAAGAGTGACATTGGTTAGGGCGA  
 TGGTTGAAGTGCGGGCAACCGCACCCAGGGATATTGGCAACGGCATAGTGGAGAACACCGT  
 GTTTTTTCATAGACGGGTTTCATCGTGCGTTGTTCACACGGTCAGCTGTTTCGATAACGCCAC  
 CTTGGTCAACAGCAACGTCAACGATACAGAGCCTGGACGCATTTGTTTGACCATCTCATC  
 TGTACCAATTCCGGTGCTTTTGCACCAGGGATGAGAATGGCTCCAATCACCACATCAGC  
 ATCTCTCATACTTGCTTCAATGTTGAATGAATTAGATATAAGAATTTGAATTTGACTTCC  
 AAAG

## ORF Predictions:

ORF #	Start	End	Direction	Length
6	59	334	R	92 aa

[SEQ ID NO: ] 3865694-6 ORF translation from 59-334,  
direction R  
VTTHDEPVYEKKGVLHYAVANIPGAVARTSTIALTNVTLPYIEALAGKGFQAISEDEGL  
RQGVTTYQGYLTSLPVAQGLNRDYTEINDLV\*

## Blastp and/or MPSearch Result:

## Description:

ALANINE DEHYDROGENASE (EC 1.4.1.1). - BACILLUS SPHAERICUS.

Assembly ID: 3865704

Assembly Length: 810bp

[SEQ ID NO: ] 3865704 Strep Assembly -- Assembly  
id#3865704

CTGCGACTAGCGGATCTCAGACAGAAGGTCAATATGGAAAAGTACATGAAAATGTGATGG  
ACTACTGGTTCAAAACGCATCCAGAAAATTTTTTCGATAATGTCGGACCTCTTGTAGCCA  
GTAACCTTTTTTCATACTTACACCGAAGATTTCCACTTGATGAAGGAAATTGGAGTTAATT  
CTTTCCGCACTTCCATCCAATGGAGTCGACTCATCAAGAATTTAGAGACAGGTGAGCCTG  
ATCCAAAAGGTATTGCTTTCTACAATGCCATTTCATGGAAGAAGCTAAAAAGAACCAGATG  
GATCTTGTGATGAATTTACATCATTTTGATTTACCAGTGGAACCTTCTTCAAAAATACGGT  
GGTTGGGAAAGCAAACATGTAGTGGAGTTATTCGTGAAGTTTGCCAAGACTGCTTTAACA  
TGCTTTGGAGATAAGGTTTCATTACTGGACAACCTTTCAATGAGCCAATGGTCATTCCAGAA  
GCAGGATACTTATATGCTTTCCATTATCCAAATCTAAAAGGAAAGGGAAAAGAGGCCGTA  
CAAGTCATCTATAATCTAAACCTTGCTAGTGCAAAAGTGATTCAACTATATCGCTCATTA  
GGACTTGATGGAAAGATTGGGATTATTTTAAACTTGACACCTGCTTATCCAAGAAGTAAT  
TCTCCAGAAGACTTAGAAGCAAGTCGATTTACAGATGACTTCTTTAACAAGTCTTCCTT  
GAATCCAGCTGTTAAAGGAACTTTCCCAGAAAAGATTGGTAAAAACAGCTAGAGAGAGAT  
GGCGTGTTATGGAGTCATACCGAAAAAGAG

## ORF Predictions:

ORF #	Start	End	Direction	Length
6	232	735	F	168 aa

[SEQ ID NO: ] 3865704-6 ORF translation from 232-735,  
direction F  
VS LIQKVLLSTMPFMEEAKKNQMDLVMNLHHFDLPVELLQKYGGWESKHVVVELFVKFAKT  
ALTCFGDKVHYWTTFNPMVIPEAGYLYAFHYPNLKGKGKEAVQVIYNLNLASAKVIQLY  
RSLGLDGKIGIILNLTPAYPRSNSPEDLEASRFTDDFFNKVFLESSC\*

## Blastp and/or MPSearch Result:

## Description:

BETA-GLUCOSIDASE A (EC 3.2.1.21) (GENTIOBIASE) (CELLOBIASE)  
(BETA-D- GLUCOSIDE GLUCOHYDROLASE). - CLOSTRIDIUM  
THERMOCELLUM.

Assembly ID: 3865788

Assembly Length: 437bp

[SEQ ID NO: ] 3865788 Strep Assembly -- Assembly  
id#3865788  
AATTCGCGTATCTCCCTCTTCCCTAACGATTGCTGAAAAATGAGTGGAGGAAAGTTTAAT  
ACCATTTCTCCAGTGTAATGGTAAATTCCTCTTTCGAAACATTTTTTATCATTACTCCTGC  
CCGTTTGTTTACGATATCAGTAGTATAAAATCGACCCTCTCCCCAAAAGAAATTACGTCT  
TACATTTTTATTTTCAATTTTCATATAAACTACTCTCTCAACTCAATTTTGATTACGCTA  
TCAATCAAGTCTGGTAATGGATAGGTAAAATGTGGAACCTTCTCCAACTGTGCAAAACAA  
ATTCTTTGTAGGCATTGGTCGTCAGCTTTCTGAAATTTTCACCTCACTTCCATCATGA  
AGAAAGCTCATTCTTTTACGTTTTCTTTACTAATAACCAAGAAGAGCTAAAGGACCTATA  
GGTTGTTCAAATACATG

## ORF Predictions:

ORF #	Start	End	Direction	Length
6	210	344	R	45 aa

[SEQ ID NO: ] 3865788-6 ORF translation from 210-344,  
direction R  
VKISESWTTNAYKGICFAQFGEVPHFTYPLPDLIDSVIKIELRE\*

Blastp and/or MPSearch Result:

Description:  
unknown

Provided in Table 2 is information on the direction of the ORF (forward or reverse) for each polynucleotide in Table 1. Also listed for each ORF is its start and stop codon positions (refer to the columns containing nucleotide code labeled "Start" and "Stop"). The triplet codon sequence for each start and stop codon is also shown. These codons may be shown in the sense orientation or antisense orientation, such as GTG and CAC, respectively, for start codons. The "Length" column discloses the length of each polynucleotide assembly. The direction of translation on the polynucleotide depicted is denoted by and "Forward" for forward or and "Reverse" for reverse (or being on the opposite strand from the one depicted). As indicated above, the "Assembly ID" number is a unique identifier assigned to each ORF of Table 1 and allows a correlation between the data in Tables 1 and 2.

**TABLE 2**

Quality	Assembly	ORF	Codon	Codon	Position	Position	Length	Direction
	ID	#	Start	Stop	Start	Stop		
Full	3047950	6	~CAC	TCA~	2	451	150	Reverse
Full	3049152	6	~CAC	TCA~	24	407	128	Reverse
Full	3174820	7	GTG	TAG	598	1041	148	Forward
Full	3175500	8	GTG	TAG	714	1049	112	Forward
Full	3175674	6	GTG	TAG	126	314	63	Forward

Quality	Assembly	ORF	Codon	Codon	Position	Position	Length	Direction
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	ID	#	Start	Stop	Start	Stop		
Full	3176442	6	GTG	TGA	350	478	43	Forward
Full	3176630	6	GTG	TAA	273	419	49	Forward
Full	3176662	6	~CAC	TTA~	2	226	75	Reverse
Full	3857692	6	GTG	TAA	386	634	83	Forward
Full	3857944	7	~CAC	TCA~	1332	1475	48	Reverse
Full	3858118	7	~CAC	CTA~	948	1160	71	Reverse
Full	3858152	6	~CAC	TCA~	546	836	97	Reverse
Full	3858258	6	GTG	TAA	207	722	172	Forward
Full	3858314	6	~CAC	TTA~	5	661	219	Reverse
Full	3858368	9	~CAC	TCA~	1207	1578	124	Reverse
Full	3858556	6	GTG	TAA	49	702	218	Forward
Full	3858562	6	~CAC	TTA~	14	178	55	Reverse
Full	3858656	6	GTG	TAA	245	559	105	Forward
Full	3859118	6	GTG	TGA	314	661	116	Forward
Full	3860084	6	~CAC	CTA~	294	473	60	Reverse
Full	3860172	8	~CAC	TCA~	1724	1888	55	Reverse
Full	3860242	7	GTG	TAA	573	1001	143	Forward
Full	3860282	6	GTG	TAA	288	1190	301	Forward
Full	3860296	8	~CAC	TCA~	1697	1843	49	Reverse
Full	3860406	6	GTG	TAA	148	504	119	Forward
Full	3860406	7	GTG	TAA	497	1405	303	Forward
Full	3860416	6	~CAC	TTA~	72	281	70	Reverse
Full	3860712	6	~CAC	CTA~	74	499	142	Reverse
Full	3860728	6	GTG	TAG	259	519	87	Forward
Full	3860794	6	~CAC	TTA~	184	915	244	Reverse
Full	3860830	6	GTG	TGA	176	286	37	Forward
Full	3860984	6	GTG	TAA	113	520	136	Forward
Full	3861088	6	~CAC	TTA~	46	474	143	Reverse
Full	3861138	6	GTG	TAG	42	437	132	Forward
Full	3861256	6	~CAC	TTA~	13	207	65	Reverse
Full	3861256	7	~CAC	TTA~	236	529	98	Reverse
Full	3861262	6	GTG	TGA	181	594	138	Forward
Full	3864150	7	GTG	TAA	922	1998	359	Forward
Full	3864150	8	GTG	TAG	2031	2759	243	Forward
Full	3864190	8	GTG	TAG	1259	1534	92	Forward
Full	3864204	8	~CAC	TTA~	1092	1835	248	Reverse
Full	3864212	6	~CAC	TCA~	256	1155	300	Reverse
Full	3864214	9	~CAC	TCA~	2812	3150	113	Reverse
Full	3864226	8	GTG	TAG	1992	2744	251	Forward
Full	3864242	6	GTG	TAA	376	1002	209	Forward

Quality	Assembly	ORF	Codon	Codon	Position	Position	Length	Direction
	ID	#	Start	Stop	Start	Stop		
Full	3864254	6	~CAC	CTA~	117	833	239	Reverse
Full	3864296	7	~CAC	TTA~	944	1777	278	Reverse
Full	3864296	10	~CAC	TTA~	2323	2694	124	Reverse
Full	3864300	9	GTG	TAA	2479	2823	115	Forward
Full	3864312	7	~CAC	TCA~	736	906	57	Reverse
Full	3864336	6	~CAC	TTA~	295	2232	646	Reverse
Full	3864344	8	~CAC	TTA~	1147	1503	119	Reverse
Full	3864352	6	~CAC	TCA~	303	1808	502	Reverse
Full	3864352	7	~CAC	CTA~	1818	2528	237	Reverse
Full	3864366	7	GTG	TAA	939	1670	244	Forward
Full	3864384	8	~CAC	CTA~	1717	2025	103	Reverse
Full	3864400	7	GTG	TAA	371	937	189	Forward
Full	3864416	7	~CAC	TTA~	929	1189	87	Reverse
Full	3864424	7	~CAC	TCA~	388	1008	207	Reverse
Full	3864430	7	GTG	TGA	627	1100	158	Forward
Full	3864442	7	GTG	TAA	867	1322	152	Forward
Full	3864442	8	GTG	TAA	1562	2074	171	Forward
Full	3864450	7	GTG	TAA	897	1448	184	Forward
Full	3864482	6	~CAC	TCA~	505	1170	222	Reverse
Full	3864496	6	~CAC	TCA~	1	1128	376	Reverse
Full	3864514	6	~CAC	TTA~	551	937	129	Reverse
Full	3864518	8	~CAC	CTA~	1985	2371	129	Reverse
Full	3864522	7	~CAC	TTA~	310	1458	383	Reverse
Full	3864568	6	GTG	TAA	296	493	66	Forward
Full	3864590	6	~CAC	CTA~	125	511	129	Reverse
Full	3864596	11	GTG	TAA	1915	2097	61	Forward
Full	3864624	6	GTG	TAA	446	751	102	Forward
Full	3864630	8	GTG	TAA	663	953	97	Forward
Full	3864654	9	GTG	TAA	1878	2306	143	Forward
Full	3864658	7	~CAC	TTA~	892	1029	46	Reverse
Full	3864664	7	GTG	TAG	675	1727	351	Forward
Full	3864700	6	~CAC	TTA~	480	740	87	Reverse
Full	3864706	6	~CAC	CTA~	336	626	97	Reverse
Full	3864710	6	GTG	TAA	442	972	177	Forward
Full	3864710	7	GTG	TGA	1247	1438	64	Forward
Full	3864724	6	~CAC	TTA~	133	1197	355	Reverse
Full	3864734	7	GTG	TAA	897	1601	235	Forward
Full	3864740	6	~CAC	CTA~	4	264	87	Reverse
Full	3864792	6	~CAC	TTA~	346	1149	268	Reverse
Full	3864830	6	~CAC	CTA~	515	1123	203	Reverse



Full	3864830	7	~CAC	TTA~	1134	1322	63	Reverse
Quality	Assembly	ORF	Codon	Codon	Position	Position	Length	Direction
	ID	#	Start	Stop	Start	Stop		
Full	3864848	6	~CAC	TTA~	707	1546	280	Reverse
Full	3864878	6	GTG	TAA	95	622	176	Forward
Full	3864950	6	~CAC	TCA~	198	500	101	Reverse
Full	3864954	6	GTG	TGA	414	1070	219	Forward
Full	3864962	6	~CAC	TTA~	195	602	136	Reverse
Full	3864970	7	GTG	TAA	1309	1710	134	Forward
Full	3865012	7	~CAC	CTA~	584	973	130	Reverse
Full	3865148	6	~CAC	TCA~	256	423	56	Reverse
Full	3865148	7	~CAC	CTA~	731	868	46	Reverse
Full	3865178	6	~CAC	TTA~	182	580	133	Reverse
Full	3865260	6	~CAC	CTA~	19	399	127	Reverse
Full	3865260	7	~CAC	TTA~	272	793	174	Reverse
Full	3865260	8	~CAC	TTA~	786	1073	96	Reverse
Full	3865272	6	GTG	TAA	101	193	31	Forward
Full	3865280	7	GTG	TGA	815	1204	130	Forward
Full	3865286	6	GTG	TAA	146	250	35	Forward
Full	3865326	7	GTG	TAA	100	681	194	Forward
Full	3865438	6	~CAC	TTA~	75	407	111	Reverse
Full	3865446	6	~CAC	TTA~	42	326	95	Reverse
Full	3865474	6	GTG	TAA	243	659	139	Forward
Full	3865476	6	GTG	TGA	394	603	70	Forward
Full	3865502	6	GTG	TAA	428	877	150	Forward
Full	3865694	6	~CAC	TTA~	59	334	92	Reverse
Full	3865704	6	GTG	TAA	232	735	168	Forward
Full	3865788	6	~CAC	CTA~	210	344	45	Reverse

## EXAMPLES

The examples below are carried out using standard techniques, which are well known and routine to those of skill in the art, except where otherwise described in detail. The examples are illustrative, but do not limit the invention.

**Example 1****Isolation of DNA coding for a virulence gene in *Streptococcus pneumoniae***

As mentioned above each of the DNAs disclosed herein by virtue of the fact that it includes an intact open reading frame is useful to a greater or lesser extent as a screen for identifying antimicrobial compounds. A useful approach for selecting the preferred DNA sequences for screen development is evaluation by insertion-duplication mutagenesis. This system disclosed by Morrison et al., J. Bacteriol. 159:870 (1984), is applied as follows.

Briefly, random fragments of *Streptococcus pneumoniae*, strain 0100993 DNA are generated enzymatically (by restriction endonuclease digestion) or physically (by sonication based shearing) followed by gel fractionation and end repair employing T4 DNA polymerase. It is preferred that the DNA fragments so produced are in the range of 200-400 base pairs, a size sufficient to ensure homologous recombination and to insure a representative library in *E.coli*. The fragments are then inserted into appropriately tagged plasmids as described in Hensel et al., Science 269: 400-403(1995). Although a number of plasmids can be used for this purpose, a particularly useful plasmid is pJDC9 described by Pearce et al., Mol. Microbiol. 9:1037 (1993) which carries the *erm* gene facilitating erythromycin selection in either *E. coli* or *S. pneumoniae* previously modified by incorporation of DNA sequence tags into one of the polylinker cloning sites. The tagged plasmids are introduced into the appropriate *S. pneumoniae* strain selected, inter alia, on the basis of serotype and virulence in a murine model of pneumococcal pneumonia.

It is appreciated that a seventeen amino acid competence factor exists (Havastein et al., Proc. Nat'l. Acad. Sci. USA 92:11140-44 (1995)) and may be usefully employed in this protocol to increase the transformation frequencies. A proportion of transformants are analysed to verify homologous integration and as a check on stability. Unwanted levels of reversion are minimized because the duplicated regions will be short (200-400 bp), however if significant reversion rates are encountered they may be modulated by maintaining antibiotic selection during the growth of the transformants in culture and/or during growth in the animal.

The *S. pneumoniae* transformants are pooled for inoculation into mice, eg., Swiss and/or C57B1/6. Preliminary experiments are conducted to establish the optimum complexity of the pools and level of inoculum. A particularly useful model has been described by Veber et al. (J. Antimicrobiol. Chemother. 32:432 (1993) in which  $10^5$  cfu inocula sizes are introduced by mouth to the trachea. Strain differences are observed with respect to onset of disease e.g., 3-4 days for Swiss mice and 8-10 days for C57B1/6.

Infection yields in the lungs approach  $10^8$  cfu/lung. IP administration is also possible when genes mediating blood stream infection are evaluated. Following optimization of parameters of the infection model, the mutant bank normally comprising several thousand strains is subjected to the virulence test. Mutants with attenuated virulence are identified by hybridization analysis using the labelled tags from the "input" and "recovered" pools as probes as described in Hensel *et al.*, Science 269: 400-403(1995). *S. pneumoniae* DNA is colony blotted or dot blotted, DNA flanking the integrated plasmid is cloned by plasmid rescue in *E. coli* (Morrison *et al.*, J. Bacteriol. 159:870 (1984)) and sequenced. Following sequencing, the DNA is compared to the nucleotide sequences given herein and the appropriate ORF is identified and function confirmed for example by knock-out studies. Expression vectors providing the selected protein are prepared and the protein is configured in an appropriate screen for the identification of anti-microbial agents. Alternatively, genomic DNA libraries are probed with restriction fragments flanking the integrated plasmid to isolate full-length cloned virulence genes whose function can be confirmed by "knock-out" studies or other methods, which are then expressed and incorporated into a screen as described above.

**What is claimed is** 1. An isolated polynucleotide comprising a polynucleotide sequence selected from the group consisting of:

(a) a polynucleotide having at least a 70% identity to a polynucleotide encoding a polypeptide comprising an amino acid sequence of Table 1;

(b) a polynucleotide having at least a 70% identity to a polynucleotide encoding a mature polypeptide expressed by the gene contained in the *S. pneumoniae* of the deposited strain that was sequenced to obtain a polynucleotide sequence of Table 1;

(c) a polynucleotide encoding a polypeptide comprising an amino acid sequence which is at least 70% identical to an amino acid sequence of Table 1;

(d) a polynucleotide which is complementary to the polynucleotide of (a), (b) or (c); and

(e) a polynucleotide comprising at least 15 sequential bases of the polynucleotide of (a), (b), (c) or (d).

2. The polynucleotide of Claim 1 wherein the polynucleotide is DNA.

3. The polynucleotide of Claim 1 wherein the polynucleotide is RNA.

4. The polynucleotide of Claim 2 comprising the nucleic acid sequence selected from the group consisting of the nucleic acid sequences set forth in Table 1.

5. The polynucleotide of Claim 2 which encodes a polypeptide comprising an amino acid sequence selected from the group consisting of the amino acid sequences set forth in Table 1.

6. A vector comprising the polynucleotide of Claim 1.

7. A host cell comprising the vector of Claim 6.

8. A process for producing a polypeptide comprising: expressing from the host cell of Claim 7 a polypeptide encoded by said DNA.

9. A process for producing a polypeptide or fragment comprising culturing a host of claim 7 under conditions sufficient for the production of said polypeptide or fragment.

10. A polypeptide comprising an amino acid sequence which is at least 70% identical to an amino acid sequence selected from the group consisting of the amino acid sequences set forth in Table 1.

11. A polypeptide comprising an amino acid sequence selected from the group consisting of the amino acid sequences set forth in Table 1.

12. An antibody against the polypeptide of claim 10.

13. An antagonist or agonist of the activity or expression of the polypeptide of claim 10.
14. A method for the treatment or prevention of disease of an individual comprising: administering to the individual a therapeutically effective amount of the polypeptide of claim 10.
15. A method for the treatment of an individual having need to inhibit a bacterial polypeptide comprising: administering to the individual a therapeutically effective amount of the antagonist of Claim 13.
16. A process for diagnosing a disease related to expression or activity of the polypeptide of claim 10 in an individual comprising:
- (a) determining a nucleic acid sequence encoding said polypeptide, and/or
  - (b) analyzing for the presence or amount of said polypeptide in a sample derived from the individual.
17. A method for identifying compounds which interact with and inhibit or activate an activity of the polypeptide of claim 10 comprising:
- contacting a composition comprising the polypeptide with the compound to be screened under conditions to permit interaction between the compound and the polypeptide to assess the interaction of a compound, such interaction being associated with a second component capable of providing a detectable signal in response to the interaction of the polypeptide with the compound;
  - and determining whether the compound interacts with and activates or inhibits an activity of the polypeptide by detecting the presence or absence of a signal generated from the interaction of the compound with the polypeptide.
18. A method for inducing an immunological response in a mammal which comprises inoculating the mammal with the polypeptide of claim 10, or a fragment or variant thereof, adequate to produce antibody and/or T cell immune response to protect said animal from disease.
19. A method of inducing immunological response in a mammal which comprises delivering a nucleic acid vector to direct expression of a polypeptide of claim 10, or fragment or a variant thereof, for expressing said polypeptide, or a fragment or a variant thereof *in vivo* in order to induce an immunological response to produce antibody and/ or T cell immune response to protect said animal from disease.
20. A polynucleotide comprising a polynucleotide sequence selected from the group consisting of the the first ten polynucleotides sequences from the top of Table 1.

21. A polypeptide comprising a polypeptide encoded by the polynucleotide of claim 20.

22. The isolated polynucleotide of claim 1 wherein said nucleotide is selected from the group consisting of:

(a) a polynucleotide having at least a 90% identity to a polynucleotide encoding a polypeptide comprising the amino acid sequence of Table 1;

(b) a polynucleotide having at least a 90% identity to a polynucleotide encoding the same mature polypeptide expressed by the gene contained in the *S. pneumoniae* of the deposited strain that was sequenced to obtain a polynucleotide sequence of Table 1;

(c) a polynucleotide encoding a polypeptide comprising an amino acid sequence which is at least 90% identical to the amino acid sequence of Table 1;

(d) a polynucleotide which is complementary to the polynucleotide of (a), (b) or (c); and

(e) a polynucleotide comprising at least 15 sequential bases of the polynucleotide of (a), (b), (c) or (d).

23. The isolated polynucleotide of claim 1 selected from the group consisting of:

(a) a polynucleotide having at least a 95% identity to a polynucleotide encoding a polypeptide comprising the amino acid sequence of Table 1;

(b) a polynucleotide having at least a 95% identity to a polynucleotide encoding the same mature polypeptide expressed by the gene contained in the *S. pneumoniae* of the deposited strain that was sequenced to obtain a polynucleotide sequence of Table 1;

(c) a polynucleotide encoding a polypeptide comprising an amino acid sequence which is at least 95% identical to the amino acid sequence of Table 1;

(d) a polynucleotide which is complementary to the polynucleotide of (a), (b) or (c); and

(e) a polynucleotide comprising at least 15 sequential bases of the polynucleotide of (a), (b), (c) or (d).

24. An isolated polynucleotide comprising a polynucleotide sequence selected from the group consisting of:

(a) a polynucleotide having at least a 50% identity to a polynucleotide encoding a polypeptide comprising the amino acid sequence of Table 1 and obtained from a prokaryotic species other than *S. pneumoniae*;

(b) a polynucleotide encoding a polypeptide comprising an amino acid sequence which is at least 50% identical to the amino acid sequence of Table 1 and obtained from a prokaryotic species other than *S. pneumoniae*; and

(c) a polynucleotide which is complementary to the polynucleotide of (a) or (b).

25. An isolated Streptococcal polypeptide having one of the amino acid sequences given in Table 1.

26. An isolated nucleic acid encoding one of the amino acid sequences of Claim 1 and nucleic acid sequences capable of hybridizing therewith under stringent conditions.

27. Recombinant vectors comprising the nucleic acid sequences of Claim 26 and host cells transformed or transfected therewith.

28. A method of identifying an antimicrobial compound comprising contacting candidate compounds with a polypeptide of Claim 1 and selecting those compounds capable of inhibiting the bioactivity of said polypeptide.

29. Antimicrobial compounds identified by the method of Claim 28.

30. An isolated Streptococcal polypeptide having one of the amino acid sequences given in Table 1.

31. An isolated nucleic acid encoding one of the amino acid sequences of Claim 30 and nucleic acid sequences capable of hybridizing therewith under stringent conditions.

32. Recombinant vectors comprising the nucleic acid sequences of Claim 31 and host cells transformed or transfected therewith.

33. A method of identifying an antimicrobial compound comprising contacting candidate compounds with a polypeptide of Claim 30 and selecting those compounds capable of inhibiting the bioactivity of said polypeptide.

34. Antimicrobial compounds identified by the method of Claim 33.

## INTERNATIONAL SEARCH REPORT

 International application No.  
 PCT/US97/21976

## A. CLASSIFICATION OF SUBJECT MATTER

IPC(6) : Please See Extra Sheet.

US CL : Please See Extra Sheet.

According to International Patent Classification (IPC) or to both national classification and IPC

## B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)

U.S. : 435/69.1, 320.1, 4, 252.3; 536/23.1, 23.7; 530/350, 386; 514/1, 12

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practicable, search terms used)

Dialog, APS

## C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
Y,E	US 5,695,937 A (KINZLER et al.) 09 December 1997, see entire document.	1-34
Y,E	US 5,723,320 A (DEHLINGER) 03 March 1998, see entire document.	1-34
Y,P	US 5,604,100 A (PERLIN) 18 February 1997, see entire document.	1-34
Y,P	US 5,652,128 A (JARVIK) 29 July 1997, see entire document.	1-34

☐ Further documents are listed in the continuation of Box C.
 ☐ See patent family annex.

* Special categories of cited documents:	"T" later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention
"A" document defining the general state of the art which is not considered to be of particular relevance	"X" document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone
"E" earlier document published on or after the international filing date	"Y" document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art
"L" document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)	"&" document member of the same patent family
"O" document referring to an oral disclosure, use, exhibition or other means	
"P" document published prior to the international filing date but later than the priority date claimed	

Date of the actual completion of the international search

12 MARCH 1998

Date of mailing of the international search report

02 APR 1998

 Name and mailing address of the ISA/US  
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**INTERNATIONAL SEARCH REPORT**

International application No.  
PCT/US97/21976

**A. CLASSIFICATION OF SUBJECT MATTER:**

IPC (6):

C07H 21/02, 21/04; C12N 15/00; C12P 21/00; C07K 14/00; A61K 35/14, 38/00; C12Q 1/00

**A. CLASSIFICATION OF SUBJECT MATTER:**

US CL :

435/69.1, 320.1, 4, 252.3; 536/23.1, 23.7; 530/350, 386; 514/1, 12